

2) INFORMATION FOR SEQ ID NO: 158

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

20 CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
 TGAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
 ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
 25 GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG 500
 30 ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
 GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT 750
 35 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGGTCTG CGTTTCGCAA 830

40 2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

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55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
 60 TGAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200

	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGTGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
5	CGCGGTATCA	TCAAAGTGGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGTTGG	500
	ACGAAGGCCG	TGCCCGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
10	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

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2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*

30 (B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTGAGGTA	GGCGTTCGGT	ACATTATCGT	GTTCTTGAAC	100
35	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCAA	200
	TCGTTCGTGG	TTCTGCTCTG	AAAGCGTCTG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
40	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAARCTGCTG	GACGAAGGCC	500
	GTGCWGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
45	CAAGTTCGAA	TCTGAAGTGT	ATATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

50

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 5 serotype Heidelberg
 (B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

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10  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
15  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG      500
20  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA YACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA TTGCCGGAAG GCGTAGAGAT      750
25  GGTAAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                        832
  
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30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
 40 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

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45  CCTGGTTGTT GCTGCGACTG ACGGCCCCGAT GCCGCAGACC CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGCTG TAGAAATGGA      150
    AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA      200
50  TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
55  GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
    GTGCTGGCGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC      650
    ATACTCCGTT CTTCAAAGGC TACCGTCCGC AATTCTACTT CCGTACGACT      700
60  GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC      750
  
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GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

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2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG C GACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA C GACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TG TAGAGCGC 400
30 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAACTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT C TACTTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAATG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGACGA CGGTCTGCGT TTCGCAA 827

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2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC 100
60 AAATGCGACA TGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCGA	200
	TCGTGCGTGG	TTCCGCTCTG	AAAGCGCTGG	AAGGCGAMGC	TGAGTGGGAA	250
	GMGAAAATCA	TCGAACTGGC	TGGCTWCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
5	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAACCTGCTG	GACGAAGGCC	500
	GTGCCGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
10	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

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2) INFORMATION FOR SEQ ID NO: 165

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 832 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 - 30 serotype Typhi
 - (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

35	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
40	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
45	ACGAAGGCCG	TGCNNGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACY	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
50	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

55 2) INFORMATION FOR SEQ ID NO: 166

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
 - (B) TYPE: Nucleic acid
 - 60 (C) STRANDEDNESS: Double

100

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

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10 CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC      50
   GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA      100
   TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAAC TGGT      150
   AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG      200
15 ACCTGCCGGT TGTTCTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT      250
   GAGTGGGAAG CTAAATCAT CGAGCTGGCC GGTCACCTGG ATTCTACAT      300
   CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG      350
   ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTTGAG      400
   CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
20 CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG      500
   ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG      550
   CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA      600
   GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG      650
   GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
25 CGTACAAC TGACGTGACCG TACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
   GGTAATGCCA GGCATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA      800
   TCGCTATGGA CCAAGGC                                     817

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30 2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

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   GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG      50
   TCGTCAGGTT GCGGTTCTT TCATCATCGT ATTCATGAAC AAATGCGACA      100
   TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAAATGGA AGTTCGTGAA      150
50 CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCTGTTG      200
   TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAATCA      250
   TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCCAGAACC AGAGCGTGCT      300
   ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG      350
   TCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG      400
55 GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT      450
   ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC GTGCTGGTGA      500
   GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG      550
   GTCAGGTACT GGCTAAACCA GGTTCATCA AGCCACACAC CAAGTTCGAC      600
   TCAGAAAGTG ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT      650
60 CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAAC TACGTCGACCG      700

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GTACCATCGA ACTGCCAGAA GCGTTGAAA TGGTAATGCC AGGTGACAAC 750
 GTGAACATGG TTGTTACCTT GATCCACCCA ATCGCGA 787

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2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GCGTTCCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
 YTGGAACTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCAGAGGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 GCGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

40 2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55 GCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTC CTGGCGACGA 200
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GCGAAGCAG 250

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AGTGGGAAAGC TAAGATTGTA GAACTGGCTG AAGCGCTGGA TTCTTACATC 300
CCAGAACCAG AGCGTGCTAT CGACAAGCCG TTCCTGCTGC CAATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTTGAGC 400
GCGGTATCAT CAAAGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
5 ACCGTTAAGT CTACCTGTAC CGGTGTAGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC 550
GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCTATCAAG 600
CCGCACACCA AATTCGACTC AGAAGTGTAC ATCCTGAGCA AAGAAGAAGG 650
TGGTCGTCCAC ACGCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
10 GTACTACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG 750
GTAATGCCAG GCGATAACGT GAACATGGTT GTTACCCTGA TTCACCCAAT 800
CGCAATGGAC GACGGTCTGC GTTTCGCAA 829

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15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: DSM 4540

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

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CGGCGCAATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTT CATCATCGTA 100
TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT 150
35 AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTACGACTTC CCTGGTGATG 200
ACCTGCCGGT TGTTTCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAACCA 250
GAGTGGGAAG CTAAATCAT CGAGCTGGCT GGTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCTA TCGACAAGCC GTTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTGAG 400
40 CGCGGTATCG TTAAAGTTGG CGAAGAAGT GAAATCGTGG GTATCAAAGA 450
CACCGTTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAATGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTGGGTG TTCTGCTGCG TGGTATCAAG 550
CGCGAAGATA TCGAACGTGG TCAGGTCCTG GCTAAACCAG GTTCAATCAA 600
GCCACACACC AAGTTTGACT CAGAAGTGT CATCCTGAGC AAAGAAGAAG 650
45 GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
CGTACAAC TGACGTGACCG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGTGACAACG TGAACATGGT TGTAACCCTG ATCCACCCAA 800
TCGCGATGGA CGACGGCCTG CGTTTCGCAA 830

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50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia rubidaea*

(B) STRAIN: ATCC 27593

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
10	TCATGAACAA	ATGCGACATG	GTAGATGATG	AAGAGCTGCT	GGAAC TGGTA	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
	CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
	CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
20	CCGCACACCC	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
25	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 172

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella boydii*

40 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

	CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAC TGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAC TGGCT	GGCTTCCTGG	ATTCTTACAT	300
50	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TGCAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGFTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
50	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 173

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

40 2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
60	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250

	GCAGAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
5	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGMCCTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
10	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

15

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
40	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
45	GCGGYCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

106

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 13301

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

	TCTGCTGCTG	ACGGTCCAAT	GCCACAAACT	CGTGAACACA	TTCTTTTATC	50
	ACGTAACGTT	GGTGTACCAG	CATTAGTAGT	ATTCTTAAAC	AAAGTTGACA	100
10	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TAGAAATGGA	AGTTCGTGAC	150
	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	TAATCGCTGG	200
	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	GAAAAAATCT	250
	TAGAATTAAT	GGAAGCTGTA	GATACTTACA	TTCCAACCTCC	AGAACGTGAT	300
	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	CAATCACTGG	350
15	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	ATCAAAGTTG	400
	GTGAAGAAGT	TGAAATCATC	GGTTTACATG	ACACATCTAA	AACAACTGTT	450
	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	AAGCTGGTGA	500
	CAACATTGGT	GCATTATTAC	GTGGTGTTGC	TCGTGAAGAC	GTACAACGTG	550
	GTCAAGTATT	AGCTGCTCCT	GGTTCAATTA	CACCACATAC	TGAATTCAAA	600
20	GCAGAAGTAT	ACGTATTATC	AAAAGACGAA	GGTGGACGTC	ACACTCCATT	650
	CTTCTCAAAC	TATCGTCCAC	AATTCTATTT	CCGTACTACT	GACGTAACCTG	700
	GTGTTGTTCA	CTTACC				716

25

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 719 bases
30	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 29247

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

	TTCTTTTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTAGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TAGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
45	TAATCGCTGG	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	200
	GAAAAAATCT	TAGAATTAAT	GGAAGCTGTA	GATACTTACA	TTCCAACCTCC	250
	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTTTACATG	ACACATCTAA	400
50	AACAACCTGTT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTGC	TCGTGAAGAC	500
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCAATTA	CACCACATAC	550
	TGAATTCAAA	GCAGAAGTAT	ACGTATTATC	AAAAGACGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCTCAAAC	TATCGTCCAC	AATTCTATTT	CCGTACTACT	650
55	GACGTAACCTG	GTGTTGTTCA	CTTACCAGAA	GGTMCTGAAA	TGTAATGCC	700
	TGGTGATAAC	GTTGAAATG				719

60 2) INFORMATION FOR SEQ ID NO: 178

107

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 625 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

15	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	50
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	100
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	150
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	200
20	CAATACGAAG	AAAAAATCTT	AGAATTAATG	GAAGCTGTAG	ATACTTACAT	250
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	300
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	350
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	400
	CACATCTAAA	ACAACGTGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	450
25	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	500
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	550
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	600
	GTGGACGTCA	CACTCCATTG	TTCTC			625

30

2) INFORMATION FOR SEQ ID NO: 179

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 704 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 43300

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

	GTTGGTGTAC	CAGCATTAGT	AGTATTCTTA	AACAAAGTTG	ACATGGTTGA	50
	CGATGAAGAA	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAA	100
50	GCGAATATGA	CTTCCCAGGT	GACGATGTAC	CTGTAATCGC	TGGTTCAGCA	150
	TTAAAAGCTT	TAGAAGGCGA	TGCTCAATAC	GAAGAAAAAA	TCTTAGAATT	200
	AATGGAAGCT	GTAATACTT	ACATTCCAAC	TCCAGAACGT	GATTCTGACA	250
	AACCATTGAT	GATGCCAGTT	GAGGACGTAT	TCTCAATCAC	TGGTCGTGGT	300
	ACTGTTGCTA	CAGGCCGTGT	TGAACGTGGT	CAAATCAAAG	TTGGTGAAGA	350
55	AGTTGAAATC	ATCGGTTTAC	ATGACACATC	TAAAACAACT	GTTACAGGTG	400
	TTGAAATGTT	CCGTAAATTA	TTAGACTACG	CTGAAGCTGG	TGACAACATT	450
	GGTGCATTAT	TACGTGGTGT	TGCTCGTGAA	GACGTACAAC	GTGGTCAAGT	500
	ATTAGCTGCT	CCTGGTTCAA	TTACACCACA	TACTGAATTC	AAAGCAGAAG	550
	TATACGTATT	ATCAAAAGAC	GAAGGTGGAC	GTCACACTCC	ATTCTTCTCA	600
60	AACTATCGTC	CACAATTCTA	TTTCCGTACT	ACTGACGTAA	CTGGTGTGTG	650

TCACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
 TGAC 704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 6538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	50
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	100
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	150
25	ATGTACCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGATGCT	200
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	GAAGCTGTAG	ATACTTACAT	250
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	300
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	350
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	400
30	CACATCTAAA	ACAACTGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	450
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	500
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	550
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	600
	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTC	650
35	CGTACTACTG	ACGTAACCTG	TGTTGTTTAC	TTACCAGAAG	GTACTGAAAT	700
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC			730

40 2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55	CGGTGCGATC	TTAGTTGTAT	CTGCAGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACCA	AGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATACGACTAC	CCAGGTGACG	200
60	ATGTACCTGT	AATCTCTGGT	TCTGCGTTGA	AAGCATTAGA	AGGCGACAAA	250

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GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAAC TCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
5 CGGTTTCAAA AAAACAACAG TTACTGGTGT AGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
10 TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

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2) INFORMATION FOR SEQ ID NO: 182

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 835 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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  (A) ORGANISM: Staphylococcus capitis subsp. capitis
  (B) STRAIN: ATCC 27840

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
35 TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGATGCT 250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAAC TCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
40 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
45 GTGGACGTC CACTCCATTC TTCAGTAAC ACCGCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTGTGTAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

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2) INFORMATION FOR SEQ ID NO: 183

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 804 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

110

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Macrococcus caseolyticus*

(B) STRAIN: ATCC 13548

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

	GTATCTTAGT	AGTATCTGCT	GCTGACGGTC	CAATGCCACA	AACTCGTGAA	50
	CACATCCTTT	TATCACGTAA	CGTTGGTGTA	CCAGCATTAG	TAGTATTCTT	100
10	GAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTTGAAA	150
	TGGAAGTTCG	TGACTTATTA	TCTGAATATG	ACTTCCCTGG	TGACGATGTA	200
	CCTGTAATCG	CTGGATCTGC	TTTAAAAGCA	TTAGAAGGCG	TTGAAGAATA	250
	CGAAGACAAA	ATCATGGAAT	TAATGGACGC	AGTTGATGAG	TACATCCCAA	300
	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
15	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCA	ACTGGACGTG	TTGAGCGTGG	400
	ACAAGTTAAA	GTTGGTGAAG	AAGTTGAAAT	CATTGGTTTA	ACTGAAGAAC	450
	CAGCAAAAC	TACAGTTACA	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CTGGAGATAA	CATCGGTGCT	TTATTACGTG	GTGTTTCTCG	550
	TGAAGACGTA	CAACGTGGAC	AAGTATTAGC	TAAACCAGGT	TCAATTACTC	600
20	CACATACTAA	ATTCAAAGCT	GAAGTTTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CACTAACTAC	CGCCCTCAGT	TCTACTTCCG	700
	TACAACTGAC	GTAAGTGGTG	TAGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	AGATAACATC	GAAATGAACG	TTGAATTAAT	TTCTCCAATC	800
	GCGA					804

25

2) INFORMATION FOR SEQ ID NO: 184

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus cohnii*

40

(B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
45	GTGAACATAT	CCTTTTATCA	CGTAACGTTG	GTGTTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCAGCATTAA	AAGCTCTTGA	AGGCGACGCT	250
	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTTCAT	300
50	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	GCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATGCAAGA	450
	AGATTCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCGTTATT	ACGTGGTGTG	550
55	GCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTTCAAT	600
	TACACCACAC	ACAAACTTTA	AAGCGGAAGT	TTACGTTTTA	TCAAAAGATG	650
	AAGGTGGCCG	TCATACGCCA	TTCTTCAGTA	ACTATCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	AGGTGTTGTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAGAAAT	GGAAGTTGAA	CTAATTTCTC	800
60	CAATCGCTAT	CGAAGACGGT	ACACGTTTCT	CT		832

2) INFORMATION FOR SEQ ID NO: 185

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

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20  ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC ATCTTATTAT    50
    CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA CAAAGTTGAC    100
    ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG AAGTTCGTGA    150
    CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT GTAATCGCTG    200
    GTTCTGCATT AAAAGCATTG GAAGGCGATG CTGAATACGA ACAAAAAATC    250
25  TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAATC CAGAACGTGA    300
    TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTC TCAATCACTG    350
    GTCGTGGTAC TGTTGCTACA GGCCGTGTTG AACGTGGTCA AATCAAAGTT    400
    GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA AAACAACGTG    450
    TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCTGGTG    500
30  ACAACATCGG TGCTTTATTA CGTGGTGTTG CACGTGAAGA CGTACAACGT    550
    GGTCAAGTAT TAGCTGCTCC TGGTTCCTATT ACACCACACA CAAAATTCAA    600
    AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT CACACTCCAT    650
    TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC TGACGTAAC    699

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35

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

```

    CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC    50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA    100
55  TTCTTAAATA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT    150
    TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG    200
    ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT    250
    CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT    300
    TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG    350
60  ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA    400

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CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG ~~GTAATCCATGA~~ 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
 5 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCACAACT ATCGTCCACA ATTCTATTTT 700
 CGTACTACTG ACGTAACTGG TGTGTGTTAA TTACCAGAAG GACTGAAAT 750
 GGTATATGCT GCGGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829
 10

2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
 30 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAA AGCTTTAGAA 200
 GCGGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
 TGAATACATT CCAACTCCAG AACGTGATTG TGACAAACCA TTCATGATGC 300
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
 CGTGTGTAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
 TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
 GGTGTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
 40 TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
 AAGACGAAGG TGGACGTAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTC AAT TACCAGAAGG 700
 TACTG 705

45

2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 60 (B) STRAIN: CSG 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

	TTTTATCAG	TAACGTTGGT	GTACCAGCAT	TAGTAGTATT	CTTAAACAAA	50
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTTG	AAATGGAAGT	100
5	ACGTGACTTA	TTATCTGAAT	ACGACTTCCC	AGGTGACGAC	GTACCTGTAA	150
	TCGCTGGTTC	AGCTTTAAAA	GCTTTAGAAG	GCGATGCTCA	ATACGAAGAA	200
	AAAATCTTAG	AATTAATGCA	AGCAGTTGAT	GATTACATTC	CAACTCCAGA	250
	ACGTGACTCT	GATAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	300
	TCACTGGTCG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGTCAAATC	350
10	AAAGTTGGTG	AAGAAGTTGA	AATTATTGGT	ATCAAAGAAA	CTTCTAAAAC	400
	AACGTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	450
	CTGGTGACAA	CATCGGTGCT	TTATTACGTG	GTGTTGCTCG	TGAAGATGTA	500
	CAACGTGGTC	AAGTATTAGC	TGCTCCAGGT	TCAATTACAC	CTCACACAAA	550
	ATTCAAAGCA	GACGTATACG	TTTTATCAAA	AGATGAAGGT	GGACGTCATA	600
15	CTCCATTCTT	CACTAACTAT	CGTCCACAAT	TCTATTTCCG	TACTACTGAC	650
	GTAACGTGGT	TTGTAACTT	ACCAGAAG			678

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

35	ACCAGCATT	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
10	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC	250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
	TACAGGCCGT	GTTGAACGTG	GTCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCAAT	450
15	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTC	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
	TTATCTAAAG	ACGAAGGTGG	ACGTACACT	CCATTCTTCA	CAAACATATCG	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTT	GTTAACCTAC	650
50	CAGAAGGTAC	TGAAATGG				668

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

```

10 AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TTGAAATGGA      50
   AGTACGTGAC TTATTATCTG AATACGACTT CCCAGGTGAC GATGTACCTG      100
   TAATCGCTGG TTCAGCATTG AAAGCTTTAG AAGGCGATGC TCAATACGAA      150
   GAAAAAATCT TAGAATTAAT GCAAGCAGTT GATGATTACA TTCCAACCTCC      200
   AGAACGTGAT TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT      250
   CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      300
15 ATCAAAGTTG GTGAAGAAGT TGAAATCATT GGTATCCATG ACACTTCTAA      350
   AACAACGTGT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG      400
   AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTGTC TCGTGAAGAC      450
   GTACAACGTG GTCAAGTATT AGCTGCTCCA GGTTCATCA CACCTCACAC      500
   AAAATTTAAA GCAGACGTAT ACGTTTTATC TAAAGACGAA GGTGGACGTC      550
20 ACACTCCATT CTTCAAAAC TATCGTCCAC AATTCTATTT CCG              593

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2) INFORMATION FOR SEQ ID NO: 191

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```

40 CGGCGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
   GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      100
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG      200
   ACGTACCTGT AATCGCTGGT TCAGCTTTAA AAGCTTTAGA AGGCGATGCT      250
45 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTATAT      300
   TCCAACCTCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGTA      400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATTATTG GTATCAAAGA      450
   AACTTCTAAA ACAACTGTGA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
50 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT      550
   CGTGAAGATG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATTAC      600
   ACCTCACACA AAATTCAAAG CAGACGTATA CGTTTTATCA AAAGATGAAG      650
   GTGGACGTCA TACTCCATTC TTCTCTAACT ATCGTCCACA ATTCTATTT      700
   CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT      750
55 GGTAATGCCT GGTGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA      800
   TCGCGATTGA AGACGGTACT CGTTTCTC              828

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60 2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

15 ATGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC ACGTAACGTT 50
 GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA 100
 CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG 150
 AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATT 200
 20 AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT 250
 GCAAGCAGTT GATGACTACA TTCCAACCTCC AGAACGTGAT TCTGACAAAC 300
 CATTTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT 350
 GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT 400
 TGAAATCATC GGTTTACATG ACACTTCTAA AACAACGTGT ACTGGTGTAG 450
 25 AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT 500
 GCTTTATTAC GTGGTGTTGC TCGTGAAGAC GTACAACGTG GTCAAGTATT 550
 AGCTGCTCCT GGTTC AATTA CACCACATAC AAAATTCAA GCGGAAGTTT 600
 ACGTTTTATC TAAAGACGAA 620

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA 50
 ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGAATTATTA TCTGAATACG 100
 50 ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTAAAAGCT 150
 TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC 200
 AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTCA 250
 TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT 300
 ACAGGCCGTG TTGAACGTGG TCAAATCAA GTTGGTGAAG AAGTTGAAAT 350
 55 TATTGGTATC AAAGAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT 400
 TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA 450
 TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC 500
 TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT 550
 TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT 600
 60 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAACCTACC 650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT :

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GGTCTGTTGA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAACTTCT 400
 AAAACAACGT TTAAGTGGTG AGAAATGTTT CGTAAATTAT TAGACTACGC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTC AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTGTTT AACTTACCAG AAGG 684
 35

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 55 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

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TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
5 TTATCAAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAAGTATCG 600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC 650
CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

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10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 611 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

```

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
TGGTTCAGCT TTAAGAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100
TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
30 GACTCTGATA AACCATTGAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT 300
GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450
AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC 500
ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
CTGGTGTTGT TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
AACGTTGAAA T 611

```

40

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

```

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAACTC 50
50 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

```

	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGATT	TATTAACGTA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
5	TCCAACCTCA	GAACGTGACT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACGTGTT	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CGTTATTACG	TGGTGTGCT	550
10	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATTG	TTCTCAAAC	ACCGCCAC	ATTCTATTTC	700
	CGTACTACAG	ACGTAACCTG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
	GGTTATGCCT	GCGGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
15	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

2) INFORMATION FOR SEQ ID NO: 198

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
40	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTG	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
	AACAACGTG	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
45	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTTT	ACGTTTATC	TAAAGATGAA	GGTGGTCGTC	650
	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

50

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSG 83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	ATGGTTGACG	ATGAAGAATT	50
	ATTAGAATTA	GTAGAAATGG	AAGTTCGTGA	TTTATTAAGC	GAATATGACT	100
10	TCCCAGGTGA	CGATGTACCT	GTAATCTCTG	GTTCTGCATT	AAAAGCTTTA	150
	GAAGGCGACG	CTGACTATGA	GCAAAAAATC	TTAGACTTAA	TGCAAGCTGT	200
	TGATGACTTC	ATTCCAACAC	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	250
	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	300
	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTC	GGTGAAGAAA	TCGAAATCAT	350
15	CGGTATGCAA	GAAGAATCAA	GCAAAACAAC	TGTTACTGGT	GTAGAAATGT	400
	TCCGTAAATT	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	TGGTGCATTA	450
	TTACGTGGTG	TTTCACGTGA	TGACGTACAA	CGTGGTCAAG	TTTTAGCTGC	500
	TCCTGGTACT	ATTACACCAC	ATACAAAATT	CAAAGCGGAT	GTTTACGTTT	550
	TATCTAAAGA	TGAAGGTGGT	CGTCATACAC	CATTCTTCAC	TAACCTACCGC	600
20	CCACAATTCT	ATTTCCGTAC	TACTGACGTA	ACTGGTGTTG	TTAACTTACC	650
	AGAAGGTACT	GAAATGGTTA	TGCCTGGCGA	TAACGTTGAA	ATGGATGTTG	700
	AATTAATTTC	TCCAATCGCT	ATT			723

25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

30	(A)	LENGTH: 697 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa 18

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	AAACAAAGTT	GACATGGTTG	50
	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTTCG	TGACTTATTA	100
	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	CCTGTAATCT	CTGGTTCTGC	150
45	ATTAAGAGCT	TTAGAAGGCG	ACGCTGACTA	TGAGCAAAAA	ATCTTAGACT	200
	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	CACCAGAACG	TGATTCTGAC	250
	AAACCATTC	TGATGCCAGT	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	300
	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	TCAAATCAAA	GTCGGTGAAG	350
	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	CAAGCAAAAC	AACTGTTACT	400
50	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	CTGGTGACAA	450
	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	TGATGACGTA	CAACGTGGTC	500
	AAGTTTTCAG	TGCTCCTGGT	ACTATTACAC	CACATACAAA	ATTCAAAGCG	550
	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	GGTCGTCATA	CACCATTCTT	600
	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	TACTACTGAC	GTAACGTGGT	650
55	TTGTTAACCT	ACCAGAAGGT	ACTGAAATGG	TTATGCCTGG	CGATAAC	697

60

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCTGC ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTGACGAT  GAAGAATTAT TAGAATTAGT      150
    TGAATGGAA  GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT      300
    CCAACTCCA  GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGT      550
    GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTAC      800
    CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

35 2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG      500
  
```

ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 556
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTT 700
 5 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCAA C 831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
 20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
 TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 30 AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
 ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
 AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400
 35 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 40 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTT 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 839 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bifidobacterium longum*
 (B) STRAIN: ATCC 15707
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

```

      TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCCCAGACTC      50
      GCGAGCACGT GCTGCTCGCC CGTCAGGTTG GCGTTCCGAA GATCCTCGTC      100
5     GCCCTGAACA AGTGCGACAT GGTCGACGAT GAAGAGCTCA TCGAGCTCGT      150
      CGAAGAAGAG GTCCGCGACC TCCTCGACGA GAACGGCTTC GACCGTGACT      200
      GCCCGGTCAT CCACACCTCC GCTTACGGTG CTCTGCACGA CGACGCTCCG      250
      GACCACGAGA AGTGGGTCCA GTCCGTAAAG GACCTCATGG ACGCTGTCGA      300
      CGACTACATC CCGACCCCGG TTCACGACCT GGACAAGCCG TTCCTGATGC      350
10    CGATCGAGGA CGTCTTCACC ATCTCCGGCC GTGGTACCGT TGTCACCGGT      400
      CGTGTCGAGC GTGGCCAGCT GGCCGTCAAC ACCCCGGTCG AGATCGTTGG      450
      TATCCGTCCG ACCCAGCAGA CCACCGTCAC CTCCATCGAG ACCTTCCACA      500
      AGACCATGGA CGCCTGCGAG GCTGGCGACA ACACCGGTCT GCTTCTGCGT      550
      GGTCTCGGCC GTGACGATGT CGAGCGTGGC CAGGTTGTGG CCAAGCCGGG      600
15    CTCCGTCAAC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA      650
      AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG      700
      TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCGAGC TGCCGGAAGG      750
      CGTCGAGATG GTTCAGCCGG GCGACCACGC TACCTTCACC GTTGAGCTGA      800
      TTCAGCCCAT CGCTATGGAG GAAGGCCTGA CCTTCGCTG      839
20

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2) INFORMATION FOR SEQ ID NO: 205

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
 35 (B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

```

      CGGCGCGATC CTGGTGTGCT CGGCCGCTGA CGGCCCGATG CCGCAGACCC      50
40    GTGAGCACAT CCTGCTGTCG CGCCAGGTCG GCGTGCCGTA CATCGTCGTG      100
      TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TCGAGCTGGT      150
      CGAGATGGAA GTGCGCGAAC TGCTGAGCAA GTACGAGTTC CCGGGCGACG      200
      ACACCCCGAT CATCGCCGGT TCGGCCCGCC TGGCGCTGGA AGGCGACCAG      250
      AGCGACATCG GCGTGCCGGC CATCCTGAAG CTGGTCGACG CGCTGGACAG      300
45    CTGGATTCCG GAGCCGGAGC GTGCGATCGA CAAGCCGTTT CTGATGCCGG      350
      TGGAAGACGT GTTCTCGATC TCGGGCCCGC GCACCGTGGT GACCGGTCGT      400
      ATCGAGCGCG GCGTGATCAA GGTTGGCGAC GAAATCGAAA TCGTCGGCAT      450
      CCGTCCGGTG CAGAAGACCA CCGTGACCGG CGTTGAAATG TTCCGCAAGC      500
      TGCTGGACCA GGGTCAGGCA GGCGACAACG CTGGCCTGCT GCTGCGCGGC      550
50    ACCAAGCGTG ATGACGTCGA GCGTGCCAG GTGCTGGCCA AGCCGGGCAC      600
      GATCAAGCCG CACACCAAGT TCGAAGGCGA AGTGTACGTC CTGTGCAAGG      650
      ACGAGGGCGG CCGCCACACC CCGTTCTTCA ACGGCTACCG TCCGCAGTTC      700
      TACTTCCGCA CCACCGACAT CACCGGCGCC GCTGCACTGC CGGAAGGCGT      750
      CGAA      754
55

```

2) INFORMATION FOR SEQ ID NO: 206

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAA	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTGAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACCTAC CGTCCACAAT TCTACTTCCG 700
 TACAACCTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 5 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25 CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG 50
 CACATCCTTC TTTCACGTCA AGTTGGTGTG AAACACCTTA TCGTATTCAT 100
 GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA 150
 TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT 200
 30 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAAATA 250
 CGAAGACATC ATCATGGAAT TGATGAGCAC TGTGATGAG TACATTCCAG 300
 AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA 350
 TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
 TACTGTTTCG GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA 450
 35 TCCAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCGTAA ACAACTTGAC 500
 GAAGGTCTTG CAGGGGACAA CGTTGGTGTG CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACCTAC CGTCCACAAT TCTACTTCCG 700
 40 TACAACCTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

45

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
   TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
   TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
   AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
   TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10  GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
   TATCCAAAAA GCAGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACCTG      500
   ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAA      550
   CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
   CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15  GTGGACGTCA TACTCCATTC TTCAACAACT ACCGTCCACA ATTCTACTTC      700
   CGTACAAC TGACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
   GGTATGCCT GGTGATAACG TTACTATCGA AGTTGAATTG ATTCACCCAA      800
   TCGCCGTAGA ACAAGGTACT AC                                     822

```

20

2) INFORMATION FOR SEQ ID NO: 210

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(i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 825 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30  (vi) ORIGINAL SOURCE:
     (A) ORGANISM: Streptococcus agalactiae
     (B) STRAIN: CDCss-1073

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

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CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA      100
10  TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT      150
   TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
   ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
   AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
   TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
15  ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
   CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
   AGATATCCAA AAAGCAGTTG TTAGTGGTGT TGAAATGTTT CGTAAACAAC      500
   TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
   CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50  CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
   TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
   AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTACAC      800
   CAATCGCCGT AGAACAAGGT ACTAC                                     825

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55

2) INFORMATION FOR SEQ ID NO: 211

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60  (i) SEQUENCE CHARACTERISTICS:

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126

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
15	TGAACACATC	CTTCTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCTTCTT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTGTAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
60	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	TGTTTCTTCT	TCGTGGTATC	550

CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
 5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCACC 800
 CAATCGCCGT TGAACAAGGT ACTACAT 827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACCTCGTGA 50
 ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
 TGAACAAAGT TGAAGTGGT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
 30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCTCAG GTGATGAAAT 200
 CCCAGTTATC CAAGGTTTCT CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
 ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
 GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
 35 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
 ATCCAAAAAG CAGTTGTTAC TGGTGTGAA ATGTTCCGTA AACAAATTGGA 500
 CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
 GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT 600
 CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
 40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
 GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
 GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT 800
 TGCCGTAGAA CAAGGAACTA C 821

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus cricetus*
 (B) STRAIN: ATCC 19642

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

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GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AAACCTCGTGA      50
ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA      100
5  TGAACAAGGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA      150
ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTCCCAG GTGATGATAT      200
CCCTGTTGTT CAAGGTTTCAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG      250
CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA      300
GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT      350
10 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG      400
GTACTGTAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA      450
ATCCAAAAAG CGGTTGTAC CGGAGTTGAA ATGTTCCGTA AACAATTGGA      500
TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC      550
GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT      600
15 CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG      650
TGGACGTCAC ACTCCATTCT TCAACAATA CCGTCCACAG TTCTACTTCC      700
GTACAACTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG      750
GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT      800
CGCTGTTGAA AAAGGTACTA C                                821
20

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2) INFORMATION FOR SEQ ID NO: 215

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25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 821 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus cristatus
35  (B) STRAIN: ATCC 51100

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

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TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
40 ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
CAGTTATCCA AGGTTTCAGCT CTAAAGCTC TTGAAGGTGA TACTAAGTAC      250
GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA      300
45 ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT      350
TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
ACTGTTTCGTG TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT      450
CCAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG      500
AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT      550
50 GATGAAATCG AACGTGGTCA AGTTATCGT AAACCAGGTT CAATCAACCC      600
ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG      650
GACGTCACAC TCCATTCTTC AACAATACTACC GTCCACAGTT CTACTTCCGT      700
ACAACGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG      800
55 CCGTTGAACA AGGTACTCCT T                                821

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2) INFORMATION FOR SEQ ID NO: 216

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus downei*
(B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

15 AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC 50
TTTCACGTCA GGTTGGTGTT AAGAACCTTA TCGTCTTCAT GAACAAGGTT 100
GACTTG GTT ACCGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG 150
TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC 200
AAGGTT CAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG 250
20 ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG 300
TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA 350
CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG 400
GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC 450
AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG 500
25 CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC 550
GAACGTGGTC AAGTGTGGC TGCGCCTGGT TCGATTCAAC CACACACTAA 600
GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA 650
CTCCATTCTT TAACAAC TAC CGTCCACAGT TCTACTTCCG TACAAC TACGAC 700
GTAAC TGGT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG 750
30 TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC 792

2) INFORMATION FOR SEQ ID NO: 217

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus dysgalactiae*
(B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

50 GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT 50
CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA 100
TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC 150
CGTGACCTTC TTTCAGAATA CGATTTCCTA GGTGATGACC TTCCAGTTAT 200
CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA 250
55 TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA 300
CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT 350
CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC 400
GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA 450
GCTGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAAC TGGT 500
50 TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTC AA CGTGACGAAA 550

	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTTC	TTCAACAACCT	ATCGTCCACA	ATTCTACTTC	CGTACAACTG	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus equi* subsp. *equi*
 (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTG TAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATATGATTTT	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTC	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTAATA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

45 2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus ferus*
 (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

60

	CGGTGCAATC	CTTGTAGTAG	CTTCTACAGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTAG	GTGTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TGCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
5	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATACT	250
	GCTCAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACCGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ATGTATTCTC	AATCACAGGT	CGTGGTACTG	TAGCTTCAGG	ACGTATCGAT	400
	CGTGGTACTG	TAAGAGTCAA	CGATGAA GTT	GAAATCGTTG	GTATCAAAGA	450
10	CGAAATCACT	AAAGCAGTTG	TTACCGGTGT	TGAAATGTTT	CGTAAACAAT	500
	TGGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTGCTTCT	CCGTGGTGTG	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCATACACCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
15	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: ATCC 10558

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTCTCA	CGCCAAGTTG	GTGTAAACA	CTTGATCGTG	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAGTTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TCTTGTGAGA	ATACGACTTC	CCAGGTGACG	200
	ATCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATATGAAG	ATATCATCAT	GGAATTGATG	AACACTGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGCGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTATCG	TTAAAGTCAA	TGACGAAAATC	GAAATCGTTG	GTATCAAAGA	450
	AGAAATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTGCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGACAAAGT	ATTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTATATCCTT	ACTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTTAC	AGGTTCAATC	GAACTTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACT			826

55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	TCAAACCTCGT	GAACATATCC	50
	TTCTTTTCACG	TCAAGTAGGT	GTTAAATACC	TTATTGTCTT	CATGAACAAA	100
15	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCC	AGGTGATGAT	ATTCCAGTAA	200
	TCCAAGGTTT	AGCACTTAAA	GCTCTTGAAG	GTGATGAAAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGAA	TACTGTTGAT	GAATATATTC	CAGAACCCAGA	300
	ACGTGATACT	GACAAACCAT	TGCTTCTTCC	AGTCGAAGAT	GTATTCTCAA	350
20	TCACTGGACG	TGGTACTGTT	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	AAAGTCAACG	ATGAAGTTGA	AATCGTTGGT	ATCCGCGAGG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAATTG	GACGAAGGTC	500
	TTGCTGGAGA	TAACGTAGGG	GTTCTTCTTC	GTGGTATCCA	ACGTGACGAA	550
	ATTGAACGTG	GACAAGTTCT	TGCTAAACCA	GGTTCAATTC	ATCCACACAC	600
25	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ATACTCCATT	CTTCAACAAC	TACCGTCCTC	AATTCTACTT	CCGTACTACA	700
	GACGTTACAG	GTTCAATCGA	ACTTCCTGCA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTAACAATTG	ATGTTGAGTT	GATCCACCCA	ATTGCCGTA	799

30

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus macacae*
 (B) STRAIN: ATCC 35911

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TGGTGCTATT	CTTGTAGTAG	CTTCAACTGA	CGGTCCAATG	CCTCAAACGC	50
	GTGAACATAT	CCTTCTTTCA	CGCCAAGTAG	GTGTTAAAAA	CCTTATTGTT	100
50	TTCATGAATA	AAGTTGACTT	AGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTACAGA	ATATGATTTC	CCAGGCGATG	200
	AACTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGATACT	250
	AAGTACGAAG	ATATTATCAT	GGAATTGTTG	GATACTGTAG	ATGATTACAT	300
	CCCAGAACCA	CAACGTGATA	CTGACAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
55	ATGTTTTTCTC	TATTACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATTGAC	400
	CGTGGTACTG	TTAAGGTTAA	TGATGAAGTT	GAAATCGTTG	GTATTCTGTA	450
	CGATATTCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTCG	GTGTCCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATTGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGATCAAT	600
50	TCATCCACAT	ACTAAATTCA	AAGGTGAAGT	TTATATTCTT	ACTAAAGAAG	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as *Streptococcus mitis*)
- (B) STRAIN: ATCC 33399

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGTAAG	TGTTCCGTAA	ACAACCTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	ACAATCGAAT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	CAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
- (B) STRAIN: ATCC 25175

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTTAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTTCT	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTC	600
	AATTCAACCA	CATACTAAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
(B) STRAIN: ATCC 15912

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	G TAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCCA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCAT	GCTTCTTCCA	GTGGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTTGTTT	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCAGTTGTTA	CTGGTGTTGA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTC	TTCAACAAC	ACCGTCCACA	GTTCTACTTC	700
	CGTAAACTG	ACGTAACTGG	ATCTATCGAA	CTTCCACCAG	GAACGTGAAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ratti*
(B) STRAIN: ATCC 19645

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGCTAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAAACCTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*
15 (B) STRAIN: ATCC 10556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCCTGGTTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GTTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus sobrinus*
(B) STRAIN: ATCC 33478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

25	TG TAG TAG CT	TCTACTGACG	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
	TGCTTTCACG	CCAAGTTGGT	GTTAAGAACC	TCATCGTCTT	CATGAACAAG	100
	GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCT	AGGTGACGAC	ATTCTGTGTG	200
	TTCAAGGTTT	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
30	AAGATTATAG	AATTGATGGA	CATCGTTGAT	GATTACAATC	CAGAACCAAA	300
	ACGCGATATG	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
	AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
	AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
35	TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
	ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTC AATCC	ACCCACACAC	600
	TAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTC TACTT	CCGTACAAC T	700
	GACGTAAACTG	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

40

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus suis*
(B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

50 TGTAGTAGCT TCAACTGACG GTCCAATGCC ACAAACCTCGT GAGCACATCC 50
TTCTTTTCACG TCAGGTTGGT GTTAAACACC TTATCGTCTT CATGAACAAA 100

	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAGTTGGTTG	AAATGGAAAT	150
	CCGTGACCTT	CTTTCAGAAT	ACGATTTCCC	AGGTGATGAT	CTTCCAGTTA	200
	TCCAAGGTTC	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	GTACGAAGAC	250
	ATCGTTATGG	AATTGATGAA	CACTGTTGAT	GAGTACATTC	CAGAACCAGA	300
5	ACGCGACACT	GACAAACCAT	TGTTGCTTCC	AGTCGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTA	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	CGTGTCAACG	ACGAAATCGA	AATCGTTGGT	CTTCAAGAAG	AAAAATCTAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAACCT	GACGAAGGTC	500
	TTGCCGGCGA	TAACGTTGGT	GTGCTTCTTC	GTGGTGTACA	ACGTGATGAA	550
10	ATCGAACGTG	GTCAAGTTAT	CTCTAAACCA	GGTTCTATCA	ACCCACACAC	600
	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCGACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAACCT	700
	GACGTAACCT	GTTCAATCAA	ATTGCCAGAA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGCCG	797

2) INFORMATION FOR SEQ ID NO: 230

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 793 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus uberis*
 - (B) STRAIN: ATCC 19436
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

	TTGTTGTTGC	ATCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
35	CTTCTTTTAC	GCCAAGTTGG	TGTTAAACAC	CTTATCGTTT	TCATGAACAA	100
	AATCGACCTT	GTTGACGATG	AAGAATTGCT	TGAATTAGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	CCTACCAAGT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GAATTGATGA	AACTGTTGA	TGAGTATATT	CCAGAACCAG	300
40	AACGTGATAC	AGACAAACCA	TTACTTCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACAGGTC	GTGGTACTGT	AGCTTCAGGA	CGTATCGATC	GTGGTACTGT	400
	TCGTGTCAAC	GACGAAATTG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	450
	AAGCAGTTGT	TACTGGTGT	GAAATGTTCC	GTAAACAACCT	TGACGAAGGT	500
	CTTGCAGGAG	ATAACGTAGG	TATCCTTCTT	CGTGGTGTTC	AACGTGACGA	550
45	AATCGAACGT	GGACAAGTTA	TTGCTAAACC	AGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGATGA	AGGTGGACGT	650
	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTATT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACTTCCAGC	TGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	AGCGTTGAGT	TGATCCACCC	AAT	793

2) INFORMATION FOR SEQ ID NO: 231

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus vestibularis*
 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

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10 TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
   CTTCTTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA      100
   AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA      150
   TCCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA TATTCCAGTT      200
   ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
   CATCATCATG GACTTGATGA ACACTGTTGA CGAATACATT CCAGAACCAG      300
15 AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA      350
   ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTGTG      400
   TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA      450
   AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAAC TACGAAGGT      500
   ATTGCCGGAG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA      550
20 AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCACACA      600
   CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT      650
   CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC      700
   TGACGTAACA GGTTCATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC      750
   CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG      798
25

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2) INFORMATION FOR SEQ ID NO: 232

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Tatumella ptyseos*
 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

```

45 GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
   TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
   TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TCCGTGACCT GCTGTACAG TACGACTTCC CGGGTGACGA      200
   CACGCCAATC GTTCGCGGT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG      250
   AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA      350
   CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC      400
   GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
55 GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA      600
   CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT      800
50 CGCGATGGAC GATGGTCTGC GTTTCGCAA      829

```


2) INFORMATION FOR SEQ ID NO: 233

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGATGA	200
	CACGCCGATC	GTACGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
25	AGTGGGAAGC	GAAAATCATC	GAAGTGGCAG	GTTTCCTGGA	TTCTTACATT	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CAACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

40 2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55

55	CGGCGCTATC	TTGGTTGTAT	CCGCAGCTGA	CGGCCCTATG	CCTCAAAGTC	50
	GCGAACACAT	CTTGTTGGCT	CGCCAAGTTG	GTGTTCTTGC	AATCGTAGTA	100
	TTCTTGAACA	AAGCTGACAT	GGTTGACGAT	GAAGAATTGA	TCGAATTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTTTCTTC	CTACGAATTC	CCTGGCGACG	200
60	AAGTACCTAT	CGTTGTAGGT	TCCGCGTTGA	AAGCTTTGGA	AGGCGATGCT	250

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	A ⁻ CTCCTACAT	300
	CCCAACACCA	GTTCGTGACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTTAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTC	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

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2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTGGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCTA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGCTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGGTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGACTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACCAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCTCAGTT	CTACTTCCGT	700
	ACAACCTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

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2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DN A

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia frederiksenii*

(B) STRAIN: ATCC 33641

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

	GGCGCGATCC	TGGTTGTTGC	TGCCACTGAT	GGCCCGATGC	CACAGACTCG	50
	CGAGCACATT	CTGTTAGGGC	GTCAGGTGGG	TGTTCTTAC	ATCCTGGTCT	100
10	TCCTGAACAA	ATGTGACATG	GTTGACGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAAC	TCTGTCTCAG	TACGATTTC	CTGGCGACGA	200
	CACTCCAGTT	ATCCGTGGT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	AAAAATCATC	GAATTGGCTG	AGGCGCTGGA	TAGCTATATT	300
	CCACAGCCAG	AGCGTGCGAT	TGATAAACCA	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTCACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTCGGC	GAAGAAGTCG	AAATCGTTGG	TATCATTGAT	450
	ACCATCAAGA	CTACCTGTAC	TGGTGTGAA	ATGTTCCGCA	AATTGCTGGA	500
	CGAAGGCCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTACGT	GGTACTAAAC	550
	GTGATGACGT	ACAACGTGGT	CAGGTATTGG	CAAAACCAGG	TTCTATCAAG	600
20	CCACACACCA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGCCAT	ACTCCGTTCT	TCAAAGGTTA	TCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTGATGCCAG	GTGATAACAT	TCAAATGATT	GTAAACCTGA	TTGCTCCTAT	800
25	CGCAATGGAT	GACGGTCTGC	GCTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 237

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

	CTTGGTTGTC	GCTGCAACTG	ATGGTCCTAT	GCCACAGACT	CGCGAGCACA	50
45	TCCTGCTAGG	TCGTCAGGTG	GGTGTTCCTT	ACATCCTGGT	CTTCCTGAAC	100
	AAGTGTGACA	TGGTTGACGA	TGAGGAGTTG	CTGGAATTGG	TAGAAATGGA	150
	AGTCCGCGAA	CTTCTGTCTC	AATATGATTT	CCCTGGCGAT	GATACTCCTG	200
	TTATCCGTGG	TTCAGCGCTG	AAGGCGTTGG	AAGGCGAGCC	TGAATGGGAA	250
	GCAAAAATTA	TCGAATTAGC	TGAGGCGCTG	GATAGTTATA	TTCCACAGCC	300
50	AGAGCGCGCG	ATTGATAGAC	CATTCTTGCT	GCCAATCGAA	GACGTATTCT	350
	CTATCTCAGG	TCGTGGTACA	GTCGTCAC	GTCGTGTAGA	GCGTGGGATC	400
	GTAAAGTTG	GCGAAGAAGT	TGAAATCGTT	GGTATTATCG	ATTCCATTAG	450
	AACAACATGT	ACTGGCGTTG	AAATGTTCCG	CAAATTGCTG	GACGAAGGCC	500
	GCGCGGGTGA	GAACGTTGGT	GTTCTACTGC	GTGGGACTAA	ACGTGATGAC	550
55	GTACAGCGTG	GTCAGGTATT	AGCTAAGCCA	GGTTCTATCA	AGCCACATAC	600
	TAAATTTCGAA	TCCGAAGTTT	ATATTCTGAG	CAAAGATGAA	GGCGGGCGTC	650
	ACACGCCGTT	CTTCAAAGGC	TACCGTCCTC	AGTTCTACTT	CCGTACAACG	700
	GATGTAACCG	GTAATATTGA	ATTGCCAGAC	GGCGTTGAGA	TGGTGATGCC	750
	AGGTGATAAC	ATTCAAATGA	TTGTAAACCT	GATTGCACCT	ATTGCGATGG	800
50	ATGATGGTCT	GCG				813

2) INFORMATION FOR SEQ ID NO: 238

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

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20  GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG      50
    TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT      100
    TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT      150
    GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTC CAGGCGACGA      200
    CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG      250
25  AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT      300
    CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA      350
    CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAGAAG      400
    GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT      450
    ACGATTAAAA CAACTTGTA TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA      500
30  TGAAGGCCGT GCTGGTGAAA ATGTTGGTGT TCTGCTGCGT GGTACTAAGC      550
    GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG      600
    CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
    CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC      700
    GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG      750
35  GTCATGCCTG GTGACAACGT AAACATGTTT GTTAACCTAA TTGCTCCTAT      800
    CGCAATGGAT GATGGTCTGC GCTTCGCAA                                829
  
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40 2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

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55  TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC      50
    GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATA CATTATTGTC      100
    TTCCTGAACA AATGTGACAT GGTTGACGAT GAAGAGTTGC TAGAGTTGGT      150
    TGAAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCAGGCGACG      200
60  ACACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT      250
  
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	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ATAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCTATTG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGATTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

2) INFORMATION FOR SEQ ID NO: 240

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Yersinia rohdei*
- (B) STRAIN: ATCC 43380

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCCCTA	CATCTTAGTC	100
	TTCCTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCTGGCGATG	200
	ACACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAACTTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTAAG	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTTGCA			829

50

2) INFORMATION FOR SEQ ID NO: 241

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yokenella regensburgei*

(B) STRAIN: ATCC 35313

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GTTTCGTGCTA	TCGACCTGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGCACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
20	GCCGCACACC	AAATTCTGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGC					804

25

2) INFORMATION FOR SEQ ID NO: 242

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

40

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45	TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
	CCGACGAGGG	TTCCTCGTTC	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
	CAACAGCTGG	GCGACGGCGT	GGTGCGTACC	ATCGCGCTGG	GCTCCAGCGA	150
	CGGCCTGCGC	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
	TGCCGGTCCG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTCGT	250
50	CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
	CCAGCCGGCT	CCCCGTTTCG	ACGAACGTCT	GCCGTCGGTG	GAAGTGTGG	350
	AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTCGC	CAAGGGCGGC	400
	AAGGTCGGCC	TGTTCGGCGG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
	GGAAGTATC	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTCG	500
55	CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
	GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTCG	GTCAGATGAA	600
	CGAACCCCCG	GGCAACCGTC	TGCGCGTGCC	GCTGACCGGC	CTGACCATGG	650
	CCGAGAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGACAAC	700
	ATCTACCGCT	ACACCCTGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCCG	750
60	TATGCCGTCTG	GCAGTGGGCT	ACCAGCCAC	GCTGGCCGAA	GAAATGGGCA	800

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAAC TGGTGATGGT GTTGTTTCGTA 50
CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAAC T 100
AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
TTGCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCGGT GGTGCTGGTG 350
TTGGTAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
30 TAATGACTTC TATCACGAAA TGAAAGATT TAACGTTCTT GACAAAGTAG 500
CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
GCGTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
GCGTATTACA TCTACTAAAT CTGGTTTCGAT CACTTCG 787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
(B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAAC TACATT 50
AGAAGTTT CAG CAACAAC TTG GTGATGGCGT AGTTTCGTACT ATTGCAATGG 100
GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
50 TCTTGGTTCG CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTTCCGGTG	TGCCGGTGTT	GGTAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTCG	CTGGTGTGG	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTTC	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTACTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG-197

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATACGT	CAAGAACATG	GTGGTATTTC	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*

(B) STRAIN: ATCC 15554

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

	TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
	CGAAAGTTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
10	AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
	CTGCGCCGCG	GTATGGAAGT	GGCCGGTTCG	GGCGCTCCCA	TCTCCGTTCC	200
	CGTGGGTGTC	GGCACCCTGG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
	TTGACGAAGT	CGGTCCTATT	CAGTCCGACG	AGCGTCGCGC	CATTACACCAG	300
	CCTGCGCCTA	CTTTCGACGA	ACTGTCGCCT	TCCGTAGAGC	TGCTGGAAAC	350
15	CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTCGCCAAG	GGTGGTAAGG	400
	TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
	CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCGG	500
	TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
	ATGCTGGCGT	TATCCAGATG	GACAACCTGA	GCGAGTCCAA	AGTGGCCATG	600
20	GTGTTGCGTC	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
	GTCCGGCCTG	ACCATGGCCG	AGAAGTTCCG	TGACGAAGGC	CGTGACATCC	700
	TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCGG	TACAGAAAGT	750
	TCCGCTCTGC	TGGGTCGTAT	GCCTTCCGCA	GTGGGTACC	AGCCTACGCT	800
	GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
25	G					851

2) INFORMATION FOR SEQ ID NO: 247

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

15	GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
	CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
	TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCAC	AGATGGACTT	150
	GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
	TGGTAGTGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
50	ACTTAGATGG	TGAGGTTTCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
	CAAGCACCTG	CATTGCAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
	TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
55	TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
50	ATGCCATCTG	CGGTAGGTGA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800

5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGTG CACAGAAGTA 150
GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
25 ACGTGTATTG AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAACTTC 250
CTGCGGATGT ACACCGTGAT CCAATTACCC GTCAAGCACC TGCATTTCGAA 300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
30 CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
AAACTGCGAT GGTATTTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
CGTGTTGCAT TAACAGGTTT AACAATGGCT GAGCATTTCG GTGATGAGCA 650
AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TCGGGTAGGT 750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
ATCTACAAAT 810

40 2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TCGCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCG	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTC	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAATACTG	GTTGTAGAAG	TTCAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAT	400
	CGGTTTGTTT	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACCTGGG	TCTTTCGAAA	GTGGATTATA	ACGAACCTGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGACTGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

55

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases

50

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCCTGGG	CCGTATCATG	AACGTCTTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAAC	GCTGGAAACC	GGCATCAAAG	350
20	TTATCGACCT	GATGTGTCCG	TTCGCGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTCG	TGACGTACTG	CTGTTCGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
	TCACCTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

30

2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGACAGCTG	GGCGACGGCG	TGGTGCCTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGGTCG	GCGCCGGCAC	CCTGGGCCGC	ATCATGGACG	TGCTGGGGCCG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACCGCGCTGC	GCCGTCGTAT	GAAGACCAGT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCCCGTTCG	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCCGGC	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAAGTATG	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCTTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTCC	CCCTGACCGG	CCTGACCATG	600

	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTT	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCCGC	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

15

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

152

	TTCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
	TTGMGGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
5	AAGCCGACTG	ACGGCCTTGT	GCGTGGCGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCgatctct	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTCGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTCGACC	AGCTGGAGTC	350
	CAAGACCCAG	ATGTTCGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
10	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	GTGTTGCGAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
15	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCAGTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
20	GACACTCCAT	CACCTC				866

2) INFORMATION FOR SEQ ID NO: 255

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
 - 35 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
40	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTGCGCGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCGATC	ATGGTGCCGG	TCGGCGTCGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
45	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTTCTCA	TCATGGAACT	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTGCGAGGCG	TCGGTGAGCG	TACCCGTGAG	500
	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
50	CGGCGGCGAA	GGCTCCAAGG	GATCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCGC	GTTGCCCTTT	CCGGTCTGAC	GGTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTCGTGG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
55	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```

15  CGAGTTCCCT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTTCT TCCGACGGTC TGCGTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCCTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
20  GGCGATATCG GCGAAGAAGA CCGTTGGGCT ATTCACCGCG CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAAC TCTGGAAGAC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGCGG GCGTGGGTAA AACCCTAAAC ATGATGGAGC TTATCCGTAA      450
    CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC      500
25  GTACTCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCGTG      650
    ACGAAGGTCT TGACGTTCTG CTGTTCTGTTG ATAACATCTA CCGTTACACC      700
    CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCTGTATG CTTCTGCGGT      750
30  AGGTTACCAG CCAACTCTGG CCGAAGAGAT GGGTGTTCTT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                                833
  
```

2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTCTTCCG ACGGTCTGCG TCGTGGTCTG      150
    GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
55  TCTGGGTCTG ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATT ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAAGTCTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTCCGTG      400
    GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
50  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
  
```

TCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGACTCC AACGTTCTGG 550
 ACAAAGTTGC ACTGGTTTAC GGCCAGATGA ACGAGCCGCC AGGTAACCGT 600
 CTGCGCGTAG CGCTGACCGG TCTGACCATC GCGGAGAAAT TCCGTGACGA 650
 AGGCCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700
 5 CCGGTACAGA AGTTTCTGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGT 750
 TATCAGCCTA CTCTGGCAGA AGAGATGGGT GTTCTTCAGG AGCGTATTAC 800
 CTCACCAAG ACCGGTTCCA TCACTTCCG 829

10

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

TCCCTCAGGA CGGCGTACCG CGCGTTTATG ACGCGCTTGA GGTACAGAAC 50
 AACAAATGAGA AGCTGGTGCT GGAAGTTCAG CAGCAGCTCG GCGGCGGTAT 100
 CGTGCGTACC ATCGCAATGG GTTCTTCCGA CCGTCTGCGT CGTGGTCTGG 150
 30 TAGTAACAGA CCTCGAGCAC CCGATCGAAG TCCCGGTAGG TAAAGCGACC 200
 CTTGGCCGTA TCATGAACGT GCTGGGTCAG CCGATCGACA TGAAAGGCGA 250
 CATCGGCGAA GAAGACCGTT GGGCGATTCA CCGCGCAGCA CCTTCCTACG 300
 AAGAGCTGTC CAGCTCTCAG GAATTGCTGG AAACCGGCAT CAAAGTTATC 350
 GACCTGATTT GTCCGTTTCG TAAGGGCGGT AAAGTAGGTC TGTTCCGGTGG 400
 35 TGCGGGCGTA GGTA AAACCG TAAACATGAT GGAGCTGATC CGTAACATTG 450
 CGATCGAGCA CTCCGGTTAT TCCGTGTTTG CGGGCGTGCG TGAGCGTACT 500
 CGTGAGGGTA ACGACTTCTA CCACGAAATG ACCGACTCCA ACGTTCTGGA 550
 TAAAGTAGCA CTGGTTTACG GCCAGATGAA CGAGCCACCA GGTAACCGTC 600
 TGCGCGTAGC GCTGACCGGT CTGACCATCG CGGAAAAATT CCGTGACGAA 650
 40 GGCCGCGACG TTTTGCTGTT CGTTGATAAC ATCTACCGTT ATACCCTGGC 700
 CGGTACCGAA GTATCTGCAC TGCTGGGTCG TATGCCTTCT GCGGTAGGTT 750
 ATCAGCCAAC TCTGGCAGAA GAGATGGGTG TTCTTCAGGA GCGTATTACC 800
 TCCACCAAGA CCGGTTCTAT CACCTCCGTA 830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAACATT	TATGACGCAC	TTGAAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCGCAG	GAGTAGGTGA	500
	GAGAACAAGA	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTCT	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGAG	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACCTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACTCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

25 2) INFORMATION FOR SEQ ID NO: 260

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter amalonaticus*

(B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAAGT	GGTCTGTTCG	300
	GTGGTGCGGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTT	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCGT	GACGTACTGC	TGTTTCGTCA	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCTGGC	GGAAGAGATG	GGTGTCTGCT	AGGAACGTAT	700
55	CACTTCTACC	AAAACCGGTT	CTATCA			726

50 2) INFORMATION FOR SEQ ID NO: 261

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
    CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
20  AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
    TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTA CTC GTGAGGGTAA      500
25  CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTT GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
    TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC      750
30  CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC      800
    CGGTTCTATC AC                                     812
  
```

35 2) INFORMATION FOR SEQ ID NO: 262

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTA GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCCTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
55  TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTCTG      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAAACC      400
    GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
50  CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT      500
  
```

ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
 GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
 CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
 TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
 5 CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
 AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAAA ACCGGTTCTA 800
 TCACCTCCGT A 811

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
 GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
 CCATCGCGAT GGGTTCCTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
 30 GACCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CTCTGGGTCTG 200
 TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
 AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
 TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
 35 TAGGTAAAC CGTAAACATG ATGGAAGTCA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
 40 CGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
 AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
 ACCCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CTTCTACCAA 800
 AACCGTTTCT ATTACC 816

45

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```

AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG      100
5  TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA      150
AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT      200
CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG      250
TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC      300
TGTC AAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG      350
10 ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCG GTGGTGCGGG      400
TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG      450
AACACTCCGG TTA CTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG      500
GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT TGGACAAAGT      550
ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG      600
15 TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT      650
GACGTTCTGC TGTTCTGTTG TAACATCTAT CGTTACACCC TGGCCGGTAC      700
AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC      750
CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC      800
AAAACCGGTT CTATCACCT                                     819
20

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2) INFORMATION FOR SEQ ID NO: 265

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 822 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Citrobacter koseri
35 (B) STRAIN: ATCC 27028

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```

GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
40 ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATCGTACGTA      100
CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA      150
GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCG      200
TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG      250
AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG      300
45 TCAA ACTCTC AGGA ACTGTT GGAA ACCGGT ATCAAAGTTA TCGACCTGAT      350
GTGTCCGTTT GCGAAGGGCG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG      400
TAGGTAA AAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA      450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG      500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
50 CTTGGTTTA CGGCCAGATG AACGAGCCGC CGGGAACCG TCTGCGCGTT      600
GCGCTGACCG CCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGTCGTGA      650
CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACGG      700
AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG      750
ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA      800
55 AACCGGTTCT ATCACCTCCG TA                                     822

```

2) INFORMATION FOR SEQ ID NO: 266

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15  GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA      50
    GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA      100
    CCATCGCCAT GGGTTCCTTC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA      150
    GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCTG      200
    TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG      250
20  AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG      300
    TCTAACTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
    GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGGT GGTGCGGGCG      400
    TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
    CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
25  TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
    CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC      600
    GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA      650
    CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG      700
    AAGTATCCCG ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750
30  ACTCTGGCGG AAGAGATGGG TGTTCGTCAG GAACGTATCA CCTCAACCAA      800
    AACCGGTTCT ATCACCTCCG                                     820
  
```

2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

50  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC      150
    CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCTGAT      200
35  CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
    AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC      300
    AGTTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
50  TCCGGTTACT CAGTGTGTTG GGGCGTTGGT GAACGTACTC GTGAGGGTAA      500
  
```

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTC					806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCCGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
35	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
40	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC					810

45

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
 (B) STRAIN: ATCC 14501

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5   TTGAGAACGG AGATTGCGG CAGCTATTGA CCGCTATTGA AATTCCTCTG   50
    AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA   100
    ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA   150
    TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA   200
    ATTCTGGGAA GAATGTTCAA TGTCTCGGA CGTGAAATTG ATGGTCTGGG   250
    ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT   300
    TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC   350
10  ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG   400
    TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA   450
    TCGCCAAGGA ACATGGTGGG ATGTCCGTCG TTACCGGTGT AGGGGAGAGA   500
    ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT   550
    TGATAAGACC GTACTGGTTF ACGGACAGAT GAATGAATCA CCGGGTGCCA   600
15  GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT   650
    CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTAC   700
    CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG   750
    TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC   800
    ATTACATCCA CGAAGGATGG TTCCATT                                827
20

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2) INFORMATION FOR SEQ ID NO: 270

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25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Clostridium perfringens
35  (B) STRAIN: ATCC 13124

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

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40  GCAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA   50
    CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA   100
    TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA   150
    GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT   200
    ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG   250
    AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT   300
45  GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT   350
    CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG   400
    GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA   450
    GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC   500
    AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA   550
50  AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA   600
    ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA   650
    AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG   700
    CTGGATCAGA GGTTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT   750
    TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC   800
55  ATCAACTACC CATGGATCAA TTACATCAG                                829

```

2) INFORMATION FOR SEQ ID NO: 271

50

(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

22

(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

CCCGCGTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
GGCGACAACC	TCGTTCCGCG	CGTGTCCATG	GCCCCTACCG	ACGGCCTCGT	150
CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
ACCACCATTG	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
CTGTTCCGGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTCATCGA	TAACATTTTC	700
CGTTTCAACC	AGGTCGGGTT	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCTCC	800
AGGAGCGTAT	TACCTCTA				818

(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

```

CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA    50
GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT    100
GATCCGGACC ATTGCGTTGG CACCTACGGA CCGTCTCGTC CGTGGCGCTG    150
10 AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC    200
AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGGACG AACCAGGATT    250
GGGCCGCGAC GGCGAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCTG    300
ATGCGCTGGA GGGCAAACC GAGATTCTGG AGACTGGAAT CAAGGTTATC    350
GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCCGTGG    400
15 CGCCGGCGTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG    450
CTCGTAACTT CTCCGGTACT TCCGTGTTTCG CCGGCGTCGG TGAGCGTACC    500
CGTGAGGGTA CTGACCTGTT CCTGGAAATG GAAGAGATGG GCGTGTGCA    550
AGACACCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTTCGTA    600
TGC GCGTGGC CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT    650
20 CAAAACCAGG ACGTTTTGTT GTTCATTGAC AACATCTTCC GTTTTACTCA    700
GGCAGGTTCC GAGGTTTCCA CGCTGTTGGG CCGTATGCCT TCCGCCGTGG    750
GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTGCA GGAACGGATT    800
ACCTCTACAC GTGGTAAGTC AATTACTTCC CTG                        833

```

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

```

CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTGGGCGGC    50
ACCTCTGTGT TCGCCGGCGT CGGCGAGCGC ACCCGTGAGG GCAACGACCT    100
15 CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT    150
TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC    200
GCGCTGACCA TGGCGGAGTA CTTCCGCGAT GTGCAGAACC AGGACGTGCT    250
GCTGTTTCATC GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT    300
CCACCCTGCT GGGCCGCATG CCCTCCGCGG TGGGCTACCA GCCGAACCTG    350
50 GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA    400
CTCCATCACC TCGATGC                        417

```

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

164

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10 GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50
 GGCAGTTGCG AAGACCATT A CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100
 ACCTGGTTCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150
 GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200
 15 TGTC AAGGGG CACGTCTTCA ACGCCCTGGG C GACTGCCTG GATGAGCCAG 250
 GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300
 TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350
 CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400
 GTGGTGCAGG TGTGGGTAAAG ACCGTCCTGA TTCAGGAGAT GATTACCCGT 450
 20 ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500
 TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC 550
 TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600
 CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650
 TGTT CAGGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700
 25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750
 GTGGGTTACC AGCCGACCTT GGCTGACGAG ATGGGTGTTT TGCAGGAGCG 800
 CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

30

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCCTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50
 AATTAAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100
 AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150
 50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT 200
 ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250
 AAAAGAAAAA TTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300
 CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350
 TGCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400
 55 TGGA AAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450
 ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500
 AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550
 GTTGGTGTA C GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600
 GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650
 50 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTTGA 700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25 TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCCTGTTG	GCAAGGCGAC	200
TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
GAAGATCTGT	CTAACTCTCA	GGAACCTGCTG	GAGACCGGCA	TTAAGGTTAT	350
30 CGACCTGATT	TGCCCCGTTG	CTAAAGGCGG	TAAAGTGGGC	CTGTTCCGGT	400
GGGCCGGTGT	GGGTAAGACC	GTTAACATGA	TGGAGCTTAT	CCGTAACATC	450
GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35 CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
AGGTCGTGAT	GTACTGTTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
CCGGTACTGA	AGTCTCCGCT	CTGCTGGGCC	GTATGCCGTC	GGCGGTAGGT	750
TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
40 CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 55 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50 ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTT	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTCATCAAT	TTGCACCTAA	GTTCCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTCGCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCCT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCCG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

55 2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10
 GCCGTACCAC GAGTGTACGA TGCACTTGAG GTAAAGAATG GTGAAGAGCG 50
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTGGCGTT GTACGTACCA 100
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCTGAT 200
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCGATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGT AAGGGCGGTA AAGTGGGTCT GTTCGGTGTT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 20 TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTAATC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
 TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 ACTGTTGTTT GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CCGTAGGTTA TCAGCCGACG 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC 800
 CGG 803

30

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
 GGTATCGTAC GACTATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG 150
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200
 CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA 250
 GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
 CTATGAAGAG CTGTCTAGCT CTCAGGAAC TCTGGAAACC GGCATCAAAG 350
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
 55 GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
 CCGTCTGCGC GTTGCGCTGA CCGGTCTGAG TATGGCTGAG AAGTTCCGTG 650
 50 ACGAAGGTCTG TGACGTACTG CTGTTCTGAG ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25 TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AAGTGTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30 TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTTG	400
GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35 CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCCTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
CGGTTCTATC					810

40

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60 CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAAC	800
15	CGGTTCTATC	A				811

2) INFORMATION FOR SEQ ID NO: 284

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
40	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
45	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTT	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTCTATC	ACTTCCG				817

55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

```

10 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT      50
   GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG      100
   TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC      150
   GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT      200
15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG      250
   AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC      300
   CTGATTTGCC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC      350
   GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA      400
   TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGGGTGA ACGTACTCGT      450
20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA      500
   AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGGA AACCCTCTGC      550
   GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT      600
   CGTGACGTTT TGCTGTTCGT CGATAACATC TACCGCTATA CCCTCGCCGG      650
   TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC      700
25 AGCCGACGCT GGCGGAAGAG ATGGGTGTTT TGCAGGAACG TATCACCTCC      750
   ACCAAAACCG GTTCTA                                     766

```

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

```

45 GCCGTACCAC GCGTGACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG      50
   CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA      100
   TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC      150
   CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT      200
50 CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG      250
   AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTACGA AGAGCTGTCC      300
   AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
55 TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA      500
   CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC      550
   TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG      600
   CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT      650
   TCTGCTGTTT GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG      700
60 TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTAA TCAGCCAACG      750

```


CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*
(B) STRAIN: ATCC 29544

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
25 GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
TTCATCGCGC GGCGCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAAGTG 300
CTGGAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
CGGTAAAGTC GGTCTGTTTC GTGGTGCAGG TGTAGGTAAA ACCGTAAACA 400
30 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTACTIONCGTG 450
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTCGTCTGA 650
35 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
GCCGTATGCC TTCAGCGGTA GGTTATCAGC CGACCCTGGC GGAAGAGATG 750
GGTGTCTTGC AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100
TGGTGTATC CGCACAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150
60 GAATGGAAGT TGTCGATACT GGCAAATCAA TCTCCGTTCC TGTAGGTAAA 200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGGG	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCGGTGGT	GCCGGTGTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTTCG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	ACGTGTTGCC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 847 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: ATCC 25788

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTGGTA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGGACA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTACTIONCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTCTGGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
50	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

50

2) INFORMATION FOR SEQ ID NO: 290

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 845 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 5 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

```

10 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCTTT AGTTGTTTAT 50
    AAAAATGATG AGAAGAAATC GAAAGTTGTT CTTGAAACAG CGCTAGAATT 100
    AGGTGACGGT GTCATCCGTA CAATCGCGAT GGAATCAACA GATGGTTTAC 150
    AACGCGGAAT GGAAGTCATT GATACAGAAA AAGCAATTTC TGTACCAGTG 200
    GGTAAAGAAA CGTTAGGTCG TGTATTCAAT GTATTAGGAG ATACGATCGA 250
    TTTATCTGCA CCTTTCCAG AAGATGCAAA ACGTAGCGAA ATCCATAAAA 300
15 AAGCACCAAA CTTTGATGAG TTAAGTACAA GTACTGAGAT CCTTGAAACT 350
    GGGATCAAAG TTATTGACTT GCTTGCTCCT TACTTAAAG GTGGGAAAGT 400
    TGGATTATTC GGTGGTGCCG GTGTAGGTAA AACTGTATTG ATCCAAGAAT 450
    TGATCCATAA TATCGCTCAA GAACACGGTG GTATTTCTGT ATTTACTGGT 500
    GTTGGTGAAC GTACACGTGA AGGTAATGAC CTTTATTATG AAATGAAAGA 550
20 TTCAGGAGTT ATTGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC 600
    CACCAGGTGC ACGTATGCGT GTTGCCTTGA CTGGTTTGAC GATTGCTGAA 650
    TACTTCCGTG ATGTTGAAGG GCAAGACGTG CTATTGTTTA TTGATAATAT 700
    TTTCCGTTTC ACTCAAGCCG GTTCAGAAGT TTCTGCCCTA TTAGGTCGTA 750
    TGCCTTCTGC CGTTGGGTAC CAACCAACGC TAGCAACAGA AATGGGTCAA 800
25 TTACAAGAAC GGATCACTTC AACGAAAAAA GGTTCAATCA CTTCA 845
  
```

2) INFORMATION FOR SEQ ID NO: 291

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

```

15 TTAGATCAAT CCTTACCCGA TATTAACAAC GCTTTAGTCG TTTATAAAAA 50
    TGGCGAAGCA AAACAAAAAG TAGTACTTGA AGTCGCTTTA GAACTAGGTG 100
    ATGGAGTGAT TCGTTCTATC GCCATGGAAT CGACAGATGG TTTACAACGT 150
    GGAATGGAAG TTATCGATAC AGGAAAATCA ATTTCAAGTT CTGTTGGTAA 200
    AGATACATTA GGTCTGTGT TTAACGTTT AGGAGACACA ATTGACTTAG 250
50 AAGCGCCATT CCCTGCAGAT GCTGAACGTA GTGGGATTCA TAAAAAGCG 300
    CCAGCATTTG ATGAATTAAG TACCAGTAAT GAAATTTTAG AAACAGGGAT 350
    TAAAGTTATT GACTTATTAG CACCTTATCT AAAAGGTGGT AAAGTCGGAC 400
    TTTTCGGTGG TGCCGGTGTT GGTAACCCG TCTTAATTCA AGAATTAATT 450
    CATAATATTG CCCAAGAACA TGGAGGGATT TCCGTCTTTA CTGGTGTG 500
55 TGAACGGACA CGTGAAGGGA ACGATCTGTA CTATGAAATG AAAGATTGAG 550
    GCGTTATTGA AAAACAGCC ATGGTTTTTG GTCAAATGAA CGAACCGCCA 600
    GGTGCACGGA TGCGTGTGGC CTTAACTGGG TTAACGATTG CTGAATATTT 650
    CCGTGATGTG GAAGGACAAG ACGTGCTATT ATTTATTGAT AACATTTTCC 700
    GTTTCACCCA AGCCGGTTCA GAAGTTTCTG CCCTTTTAGG TCGGATGCCG 750
50 TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA 800
  
```

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCTCTGTA 200
 25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
 TTTAGAAACA CCTTTCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
 GGGATCAAAAG TTATCGATT TCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
 30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
 TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
 35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
 TGCCTTCTGC GGTTGGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
 TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
 60 TCATCGATAC CCGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

175

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTCCGGTG	400
5	TGCCGGTGTT	GGTAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTTGG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGA CTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus saccharolyticus*
- (B) STRAIN: ATCC 43076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGGTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTT	TGTTCCCTGT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCACT	ATTTGCGGGT	500
	GTTGGTGAGC	GTACTCGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
15	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTCAGAAAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

50

2) INFORMATION FOR SEQ ID NO: 295

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia fergusonii*
 5 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

```

10 GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTGCAAAATG GTAATGAGCG      50
   TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGTGGTATC GTGCGTACCA      100
   TCGCAATGGG GTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAC      150
   CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT      200
   CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG      250
   AAGAGCGTTG GGCGATTAC CCGCAGCAC CTTCTACGA AGAGCTGTCA      300
15 AACTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAACTGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
   TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
   CGACTTCTAC CACGAAATGA CTGACTCCAA CGTTATCGAC AAAGTATCCC      550
20 TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA      600
   CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
   TCTGCTGTTT GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
   TATCCGCACT GCTGGGCCGT ATGCCTTCAG CGGTAGGTTA TCAGCCGACT      750
   CTGGCGGAAG AGATGGGCGT TCTTCAGGAA CGTATCACCT CCACCAAAAC      800
25 TGG                                     803

```

2) INFORMATION FOR SEQ ID NO: 296

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

```

45 GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA ATGGTGATGA      50
   GCGTCTGGTG CTGGAAGTGC AGCAGCAGCT CGGCGGCGGT ATCGTGCGTA      100
   CCATCGCAAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GACTGTCGTC      150
   GACCTCGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCGA CCCTGGGCCG      200
   TATCATGAAC GTGCTGGGTC AGCCGATCGA CATGAAAGGC GATATCGGTG      250
50 AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCGTCCTA TGAAGAGCTG      300
   TCCAGCTCTC AGGAACTGCT GGAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGCG      400
   TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
55 TAACGACTTC TACCATGAAA TGACCGACTC CAACGTTCTG GACAAAGTAT      550
   CCCTGGTTTA CGGCCAGATG AACGAACCGC CGGGAAACCG TCTGCGCGTT      600
   GCACTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGTTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACTG      700
   AAGTATCCGC ACTGCTGGGC CGTATGCCTT CTGCGGTAGG TTACCAGCCG      750
50 ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAGCGTATCA CCTCCACCAA      800

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5 2) INFORMATION FOR SEQ ID NO: 297

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
CAGGAAGTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
CGCCAAGGGC GGTAAGTTCG GCCTGTTTCG CGGCGCGGGC GTGGGTAAAA 400
CCGTAAACAT GATGGAGCTG ATCGTAACA TCGCGATCGA GCACTCCGGT 450
30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
ACGGCCAGAT GAACGAGCCG CCGGGAACC GTCTGCGCGT GGCCTGACC 600
GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
GTTCTGTTGAC AACATCTATC GTTACACCTT GGCCGGTACG GAAGTATCTG 700
35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTT 800
TATCACCT 808

40 2) INFORMATION FOR SEQ ID NO: 298

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTAC AACGCGCTGA CGGTTGATGC 50
CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
TGCCGGGCAA CTTGTCCGC TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
50 GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200

	GGGTCCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCCGTG	250
	ACGAGAAGCC	GATGCCCCGAG	GTGAAGGGCT	ACATGCCCCAT	CCACCGTCCG	300
	GCTCCGGACT	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTCGG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTCGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*

(B) STRAIN: ATCC 33852

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTGCGT	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAAC TCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTTCG	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
50	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

2) INFORMATION FOR SEQ ID NO: 300

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
 5 (B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

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AACACGCCTA AAGTATATGA TGCTTTAAAT GTAGTAGAAG CTGGTTT TAGT      50
10 ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA      100
   TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAAGTTAA GAACACAAAT      150
   GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA      200
   TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA      250
   AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAAGT      300
15 ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT      350
   TGCTAAGGGC GGTAAGTTG GTTTATTTGG CGGTGCAGGT GTTGGTAAAA      400
   CTGTAACGAT GATGGAAGTT ATCAACAATA TTGCAAAAAGA ACATAGTGGC      450
   TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT      500
   CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT      550
20 ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAGAGT AGCTCTTAGT      600
   GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT      650
   GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG      700
   CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA      750
   GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC      800
25 TATTA      805

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2) INFORMATION FOR SEQ ID NO: 301

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Fusobacterium gonidiaformans*
 (B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

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45 GACGAATTGC CAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
   AGAACTTGTA TTGGAAGTGC AACAACATTT GGGAAATAAT GTTGTGAGAA      100
   CAGTAGCGAT GGA CTCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG      150
   GATACCGGAG CACCGATTAC TGTTCCAGTA GGGAAGGCGG TTTTAGGAAG      200
   AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAG      250
50 CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA      300
   GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAAGTCA TAGATTTGTT      350
   AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCCGT GGAGCCGGAG      400
   TAGGGAAAC AGTTTTAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC      450
   CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG      500
55 AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTGT AATAAGACCT      550
   CGTTGGTGTA TGGTCAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG      600
   GCGTTGACAG GATTAACGGT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA      650
   AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT      700
   CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA      750
60 CCGAAGTTAG CGACAGAAAT GGGAAGTTTA CAAGAAAGAA TTACTTCTAC      800

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5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp. *necrophorum*
(B) STRAIN: ATCC 25286

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT AAAGGTACAG GTGGGAGAAA GGGAACTTGT GTTGGAAGTG 50
CAGCAACATT TAGGAAATAA TGTTGTCAGA ACAGTAGCAA TGGATTCAAC 100
AGACGGATTA CTTCGGGGAA TGGAAGTGAG AGATACAGGA GTTCCCATT 150
25 CTGTTCCGGT AGGAAAGGCG GTTTTGGGAA GAATATTAAA TGTCTTAGGG 200
GAGCCTGTGG ACGAAAAGG TCCGATAGAG ACAGAAGAAT ATTTACCAAT 250
ACATAGAGAA GCACCGAAAT TTGAAGAACA GGAAACGGTG ACAGAAATTT 300
TTGAAACAGG AATTAAAGTC ATTGATTGTG TAGCTCCTTA TATTAAAGGA 350
GGAAAACAG GCCTATTCGG AGGAGCCGGA GTAGGAAAAA CCGTTTGTGAT 400
30 TATGGAAC TGCAATAATA TTGCAAAAGG TCATGGAGGA ATTTCTGTTT 450
TTGCAGGAGT TGGAGAAAGA ACGAGAGAGG GAAGAGATCT ATACAACGAA 500
ATGACAGAGT CCGGAGTTTT GAATAAACT TCTTTGGTAT ATGGGCAAAT 550
GAATGAGCCG CCCGGAGCAA GACTTCGAGT GGCTTTAACC GGACTTACTG 600
TTGCCGAAAA TTTCAGAGAT AAAGAGGGAC AGGATGTCTT ATTGTTTATT 650
35 GACAATATTT TCCGTTTCAC ACAAGCAGGT TCGGAAGTAT CGGCACTTTT 700
GGGGAGAATT CTTTCTGCAG TGGGATATCA ACCGAACTTG GCGACAGAAA 750
TGGGAAGCTT ACAAGAAAGA ATTACTTCTA CAAATCCGG TTCTATCACT 800
TCCGTG 806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC CTGCAATATA TAATGCTTTA AAAGTAAAAA TAGAAGATAA 50
GGAACTTGTT CTAGAAGTTG AACAACATCT TGGTAACAAT GTTGTAAGAA 100
50 CTGTTGCTAT GGATTCAACT GATGGATTAA AAAGAGGAAT GGAAGTTATA 150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTCTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACTTA	TCAACAACAT	TGCAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCATTAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821
15						

2) INFORMATION FOR SEQ ID NO: 304

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 864 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Gardnerella vaginalis*
 - (B) STRAIN: ATCC 49145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACGCAA	CCCACCTGCT	TTCGATCAGC	TTGAGTCTAA	350
	GACTCAAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTTG	CTTACGCCTT	400
	ACGTTCAGGG	CGGAAAGATT	GGTCTGTTCG	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTCAGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACG	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTCAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCTCTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTCAGAAT	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

55 2) INFORMATION FOR SEQ ID NO: 305

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 848 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10 TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA 50
 GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT 150
 TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT 200
 15 GTAGGTAAGT ACACATTAGG TCGTGTGTTT AACGTATTAG GTGAAGCAGT 250
 TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA 300
 AAGAAGCTCC AACATTTCGAT GAATTATCAA CTCACGTTGA GGTTCTTGAA 350
 ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA 400
 AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG 450
 20 AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA 500
 GGTGTAGGTG AGCGTACTCG TGAAGGAAT GACTTATACT ATGAAATGAA 550
 AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG 600
 AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAATGGCG 650
 GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA 700
 25 CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTTCTGCG TTATTAGGAC 750
 GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA 800
 CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT 848

30 2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA 50
 GAAAAAGGCG ATGGAAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT 150
 50 TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA 200
 GTAGGTAAGT ATACATTAGG ACGTGTGTTT AACGTATTAG GTGAAGCAGT 250
 TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTCATA 300
 AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA 350
 ACAGGTATTA AAGTTATCGA CTTCTTGCA CCATATATTA AAGGTGGTAA 400
 55 GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG 450
 AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT 500
 GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTAAT ATGAAATGAA 550
 AGACTCTGGA GTTATTAATA AAACCTGCCAT GGTATTTGGT CAAATGAATG 600
 AGCCACCAGG TGCACGTATG CGTGTTCGCT TAACAGGATT AACAATGGCA 650
 50 GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA 700

TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

5

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
10 AATCACGGCA	GTA				813

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 (B) STRAIN: ATCC 33390

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCCTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTTCGCAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGCG	400
	GGTGTAGGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCGTG	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

2) INFORMATION FOR SEQ ID NO: 309

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCCATT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTTGG	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAACA	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCCT	AGCAGGTACG	GAAGTGTCAG	700
	CACTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

55 2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10 CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG 50
 AATCGGGTTT AACCCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA 100
 CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT 150
 TGAAAATACC AATAAACCAA TTTCAGTACC GGTTGGTGTA AAAACTCTCG 200
 15 GTCGTATTAT GAACGTATTG GGCGAACCGA TTGATGAAAG AGGTCCTATC 250
 GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA 300
 ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT 350
 TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG 400
 GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT 450
 20 TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG 500
 AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA 550
 GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG 600
 TGTGTCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC 650
 GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG 700
 25 ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA 750
 GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA 800
 CCAAACAGG TTCTATTACT TCTG 824

30

2) INFORMATION FOR SEQ ID NO: 311.

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA 50
 ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA 100
 TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC 150
 50 CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT 200
 TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG 250
 AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT 300
 AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTTG 400
 55 GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTA CTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC 550
 TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACTATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 60 ACTGCTGTTT ATCGATAACA TCTACCGTTA TACCTTGCC GGTACCGAAG 700

TATCTGCACT	GTTGGGTCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCAACG	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACCT	CGACCAAAAC	800
GGTTCAATC	A				811

5

2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

CGGATGCTAT	TCCACGCGTT	TACGATGCGT	TGAAACTGGT	TGATGTGGAC	50
TTGACATTAG	AAGTGCAACA	ACAACTGGGC	GATGGCGTAG	TGCGTACCAT	100
25 TGCGATGGGT	AGTACCGATG	GTTTGAAACG	CGGCTTAGCC	GTGAACAACA	150
CAGGCGCACC	TATTACAGTG	CCTGTTGGTA	AAGCAACATT	GGGTCGTATT	200
ATGGACGTAT	TGGGTAATCC	TGTTGATGAA	GCAGGTCCAA	TTGGTTCTGA	250
CCAAACGCGT	GCTATTCACC	AACCAGCTCC	TAAATTTGAT	GAACGTGCTA	300
GCGCAACCGA	ATTGCTGGAA	ACAGGCATCA	AAGTGATTGA	CTTGCTTTGC	350
30 CCATTTGCAA	AAGGTGGTAA	AGTAGGTTTG	TTTGGTGGTG	CAGGTGTGGG	400
CAAAACTGTG	AACATGATGG	AGTTGATTAA	CAACATTGCC	AAAGCGCACA	450
GTGGTTTGTC	TGTATTTGCA	GGCGTGGGTG	AACGTACTCG	CGAAGGTAAT	500
GACTTCTATC	ACGAGATGAA	AGATTCTAAC	GTGTTGGATA	AAGTTGCCAT	550
GGTGTATGGT	CAAATGAATG	AACCTCCTGG	CAACCGTTTG	CGCGTTGCAT	600
35 TGACTGGTTT	GTCTATGGCA	GAACACTTCC	GTGATGAAAA	AGACGAAAAT	650
GGCAAAGGTC	GCGATGTATT	GTTCTTTGTG	GACAACATCT	ATCGCTACAC	700
ATTGGCAGGT	ACAGAAGTAT	CGGCATTGCT	GGGTCGTATG	CCCTCTGCGG	750
TAGGTTATCA	ACCAACATTG	GCAGAAGAAA	TGGGTCGTTT	GCAAGAGCGT	800
10 ATTACTTCAA	CGCAAACAGG	TTCGATTACT	T		831

2) INFORMATION FOR SEQ ID NO: 313

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 55 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC	ACGCGTGTAC	GAAGCCCTTG	AGGTACAGAA	TGGTAATGAA	50
50 GTTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGCGGTA	TCGTACGTAC	100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCAGTCGAA	GTCCCAGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCCA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTGCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CCAAGGGCGG	TAAAGTTGGT	CTGTTCCGGC	GTGCGGGTGT	400
	AGGTAAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTTCGTGAC	650
	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella ornithinolytica*
 (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGATC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCAGTCGAA	GTCCCAGGTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAAATCGAT	ATGAAAGGCG	ACATCGGCCA	250
40	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTGCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
45	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTTCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

55 2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CCGTATTGTT CGTACCATCG 100
 CCATGGGTTT TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150
 GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200
 15 GAACGTA CTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250
 AGCGTTGGGC GATTCACCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC 350
 GTTTGCGAAG GCGCGTAAAG TTGGTCTGTT CCGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 20 GGTTACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600
 ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650
 GCTGTTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700
 25 CCGCACTGCT GGGTCGTATG CTTTCAGCGG TAGGTTACCA GCCGACTCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CAAAACGGG 800
 TTCTATCACT TCC 813

30

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50
 GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100
 CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150
 50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCTG 200
 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250
 AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300
 TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTTCGGT GGTGCGGGCG 400
 55 TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650
 60 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG 700

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCC	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGTTTCT	ATCACTTCCG	TA			822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAAC	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GGCGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTACTCGTGA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTA	CTGTTCGTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAAACCGGT	TCTATCACCT	CCGTA		785

10

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAGATC	100
50 TCGAGCACCC	AATCGAAGTT	CCGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCACCC	AGTMGACATG	AAAGGCGACA	TCGGTGAAGA	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTCGCTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTTGG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGGTTACTC	CGTGTTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTC	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTACTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GGTTCTATC					759

15

2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*

(B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTTCAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAG	ACCTCGAGCA	CCCATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
10	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	400
	GTGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAACCGT	600
15	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTAAGTCTGT	TCGTGATATA	CATCTATCGT	TACACCTTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
50	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

50

2) INFORMATION FOR SEQ ID NO: 320

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 5 (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

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10  GCCGTACCGC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAAGT    50
    GCTGGTGCTG GAAGTTCAGC AGCAGCTCGG TGGCGGTATC GTGCGTACCA    100
    TCGCCATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA AGTTAAAGAT    150
    CTCGAGCACC CGATCGAAGT TCCGGTAGGT AAAGCAACAC TGGGTCGTAT    200
    CATGAACGTA CTGGGTCACC CGGTAGACAT GAAAGGCGAC ATCGGTGAAG    250
    AAGAGCGTTG GGCTATCCAC CGCGCTGCGC CTTCCTACGA AGAGCTGTCC    300
15  AGCTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG    350
    TCCGTTCCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGCGGT GCGGGTGTG    400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC    450
    TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA    500
    CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC    550
20  TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG    600
    CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT    650
    ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG    700
    TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCGACT    750
    CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC    800
25  CGGTTCATATC                                     810
  
```

2) INFORMATION FOR SEQ ID NO: 321

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*
 40 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

```

15  TCGATAAGAA TTTACCTGAT ATTAACAACG CCTTACGTGT AATCAAGTCC    50
    GAAGATGAAA GCATCGTTCT TGAAGTTACA CTTGAACTCG GTGATGGTGT    100
    TTTAAGAACA ATCGCCATGG AATCTACCGA TGGTCTTCGT CGTGGTATGA    150
    AAGTCGAAGA TACTGGCGCT CCAATTTTCTG TTCCAGTTGG AGAAGACACT    200
    TTAGGTCGTG TGTTTAACGT TTTAGGACAG CCTATTGATG GTGGTCCAGC    250
50  CTTTCCAAAG GATCACCACG GTGAGGGTAT CCACAAGGAA GCACCTAAAT    300
    ATGAAGATTT AACTACTAGT CGTGAAATTC TTGAAACTGG TATCAAGGTT    350
    ATCGACCTTC TTGAACCATA TGTCGTGGT GGTAAAGTTG GTTTGTTTGG    400
    TGGTGCCGGT GTTGGTAAAA CTACTATTAT TCAAGAATTA ATTCACAACA    450
    TCGCTCAAGA ACACGGTGGT ATTTCCGTAT TTACTGGTGT TGGTGAAAGA    500
55  ACTCGTGAAG GTAATGACCT TTACTTTGAA ATGAAAGCTT CAGGCGTTT    550
    AAGTAAGACT GCCATGGTAT TTGGTCAGAT GAACGAGCCG CCTGGTGCCA    600
    GAATGCGTGT TGCATTAACC GGTTTGACAC TTGCTGAATA CTTTAGAGAT    650
    GTTGAAGGTC AAGACGTATT GCTCTTTATT GACAATATCT TTAGATTTAC    700
    TCAGGCTGGT TCAGAGGTAT CTGCTTTGCT TGGTCGTATG CCAAGTGCCG    750
60  TAGGTTATCA GCCAACTTTG GCAACAGAAA TGGGTCAATT GCAGGAAAGA    800
  
```

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAACTG GTATTAAAGT AATTGATTTG 350
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGT GGTCTATTCG GTGGTGCCGG 400
 TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCTG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTCGGCCT	GTTCGGCGGC	GCCGGCGTAG	400
5	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCGC	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

2) INFORMATION FOR SEQ ID NO: 324

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Listeria monocytogenes*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACTT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACTCTTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCACC	300
	GCGAAGCTCC	AACTTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCTTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGGTG	CCGGTGTTGG	TAAAACCGTT	CTAATTC AAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTT	TGTGTTTCGCT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTCAGGC	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAAGTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Micrococcus lylae*

(B) STRAIN: ATCC 27566

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA 50
 CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC 100
 10 GGCACAACT TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT 150
 CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG 200
 GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT 250
 GAGCCAGGTC TTGGCCGTGA CCGTGAGCAG TGGGGCATCC ACCGCGATCC 300
 GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA 350
 15 TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC 400
 CTGTTCCGGTGT GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT 450
 CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG 500
 GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG 550
 GGCGTTCTCC AGGACACCGC TCTTGTGTTT GGCCAGATGG ACGAGCCTCC 600
 20 AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT 650
 TCCGCGATGT GCAGCACCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC 700
 CGTTTACCCC AGGCAGGTTC CGAGGTTTCC ACCCTCCTAG GCCGCATGCC 750
 TTCTGCCGTG GGTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC 800
 AGGAGCGTAT TACCTCCACA AAGGGTAA 828
 25

2) INFORMATION FOR SEQ ID NO: 326

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moellerella wisconsensis*

40 (B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA 50
 15 AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTCGTT 100
 GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA 150
 AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGCCCG 200
 TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG 250
 AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG 300
 50 GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT 350
 TTGCCCATTG CTTAAAGGGG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG 400
 TCGGTAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG 450
 CACTCAGGTT ATTCTGTATT CGCGGGTGTG GGTGAACGTA CTCGTGAAGG 500
 TAACGATTTT TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT 550
 55 CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT 600
 GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
 CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG 700
 AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA 750
 ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA 800
 50 GACCGGCTCT ATCACTTCCG TA 822

2) INFORMATION FOR SEQ ID NO: 327

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

```

20  CCGTGGCGAT GTCCCCCAA TCTTTGATGC ACTTCATGTT GATGGTACTG      50
    AAACCACCCT TGAAGTCCAA CAACAGTTAG GTGATGGTGT GGTGCGTACC      100
    ATTGCCATGG GTTCTACCGA AGGCTTAAAG CGTGGCTTGC CTGTCTCTAA      150
    TTCAGGTGCA CCCATTTTCGG TACCAGTCGG TCAAGCAACA CTGGGTCGCA      200
    TTATGGATGT CCTAGGTCGC CCAATCGATG AAGCAGGTCC GGTAATGCT      250
25  GAACAAAAAT GGTCCATTCA TCGTGAAGCA CCAAGTTATG ATGAACAGTC      300
    AAATAGTACA GAACTTTTAG AAACAGGCAT CAAAGTGATT GATTTGCTTT      350
    GTCCATTTGC CAAAGGTGGT AAAGTCGGTC TGTTCCGGTGG TGCTGGTGT      400
    GGTAAGACCG TTAACATGAT GGAGCTTATC AATAATATCG CCCTAAAACA      450
    CTCAGGTCTG TCGGTTTTTG CTGGTGTGGG TGAGCGTACT CGTGAGGGTA      500
30  ATGACTTCTA CCATGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAT      550
    TTTACTCAGT CAAAAGTTGC CATGGTTTAT GGTGAGATGA ATGAGCCACC      600
    AGGAAACCGT CTGCGTGTG CTTAACTGG TTTGACCATG GCAGAGTATT      650
    TCCGTGATGA AAAAGACGAA GCAACGGGCA AAGGCCGTGA TGTCTGCTG      700
    TTCGTTGATA ATATTTATCG TTACACATTG GCAGGTACTG AGGTATCAGC      750
35  ACTTTTAGGT CGTATGCCAT CTGCGGTAGG TTATCAGCCG ACTTTGGCCG      800
    AAGAGATGGG CTTGCTACAA GAGCGTATCA CCTCCACCCA ATCAGGCTCA      850
    ATTA

```

40

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

```

50  CCGTCAAAGC GTACCAAGAA TTTATGATGC CTTAAAAGTT GAAGGCACAG      50
    AAATAACATT AGAAGTACAA CAACAATTGG GTGATGGTAT CGTACGTACT      100
    ATTGCCATGG GTTCTACTGA AGGTCTAAAA CGTGGTCTAC CAGTTAGCAA      150
    CACTGGCGCA CCAATCTCTG TACCTGTGGG TAAAGGTACA CTAGGTCGTA      200

```

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAACCTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTGC	TAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTG	CGCGGGTGTT	400
5	GGTAAACCG	TTAACATGAT	GGAACCTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATT	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAGA	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

2) INFORMATION FOR SEQ ID NO: 329

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTCTT	CAGGATGCAG	TACCGAAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACATCG	GCGCAGAAGA	AAAATGGTCT	ATTCACCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAACT	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCC	TTGCGGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGGTGCGG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTCGCAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAA	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTCTGTT	ATAACATCTA	CCGTTATACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGTTA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

2) INFORMATION FOR SEQ ID NO: 330

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 5 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

```

10 GACGCGGTAC CGCAAGTGTA CAGCGCCCTC GAGGTTATGA ATGGTGATGC 50
   GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGC GTAGTACGTA 100
   CCATCGCAAT GGTACGTCT GACGGCCTGA AGCGTGGTCT GAGCGTCAAC 150
   GACCTGCAGA AACCGATTCA GGTACCCGTC GTTAAAGCGA CCCTGGGCCG 200
   TATCATGAAC GTTCTCGGCG AGCCAATCGA TATGAAAGGC GAGCTGAAAG 250
   AAGAAGATGG CAGCGCAGTA GAGATCGCCT CTATTCACCG CGCAGCCCCT 300
15 TCTTATGAAG ATCAGTCTAA CTCGCAGGAA CTGCTGGAAA CCGGCATCAA 350
   GGTTATCGAC CTGATGTGTC CGTTTGCTAA AGGCGGTAAA GTCGGTCTGT 400
   TCGGTGGTGC GGGTGTAGGT AAAACCGTCA ACATGATGGA ACTGATCCGT 450
   AACATCGCGG CTGAACACTC AGGTTACTCA GTGTTTGCCG GTGTGGGTGA 500
   GCGTACTCGT GAGGGTAACG ACTTCTACCA CGAAATGACT GACTCTAACG 550
20 TTATCGATAA AGTTGCACTG GTCTATGGCC AGATGAACGA GCCGCCGGGT 600
   AACCGTCTGC GCGTAGCACT GACCGGTCTG ACCATGGCGG AAAAATTCCG 650
   TGATGAAGGT CGCGACGTTT TGCTGTTCAT CGATAACATC TACCGTTATA 700
   CCCTGGCCGG TACAGAAGTT TCTGCACTGC TGGGTCGTAT GCCATCTGCG 750
   GTAGGTTACC AGCCAACGCT GGCAGAAGAG ATGGGTGTGT TGCAGGAGCG 800
25 TATTACCTCC ACCAAGACCG GTTC 824

```

2) INFORMATION FOR SEQ ID NO: 331

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

```

45 TATACAGCGC TCTCGAGGTA AAAAATGGTG ATGCTCGTCT GGTGCTGGAA 50
   GTACAGCAGC AGCTGGGCGG TGGCGTGGTG CGTACCATCG CCATGGGTTC 100
   TTCTGACGGC CTGAAGCGCG GTCTGGAAGT CACCGACCTG AAAAAACCTA 150
   TCCAGGTTCC GGTTGGTAAA GCAACACTCG GCCGTATCAT GAACGTGCTG 200
   GGTGAGCCAA TCGACATGAA AGGCGACCTG AAAGAAGAAG ACGGCAGCGC 250
50 TGTAGAGGTT TCCTCTATTC ATCGCGCAGC GCCTTCTTAT GAAGATCAGT 300
   CAAACTCGCA GGAAGTCTG GAAACCGGCA TCAAGGTTAT CGACCTGATG 350
   TGTCGGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCTGGT GTGCGGGTGT 400
   AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGGCTGAGC 450
   ACTCAGTTA TTCGGTCTTT GCCGGCTGG GTGAGCGTAC TCGTGAGGGT 500
55 AACGACTTCT ACCACGAAAT GACGGACTCC AACGTTATCG ATAAAGTAGC 550
   GCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGTAACCGT CTGCGCGTAG 600
   CACTGACCGG TCTGACCATG GCGGAAAAAT TCCGTGATGA AGGCCGTGAC 650
   GTTCTGCTGT TCATCGACAA CATCTACCGT TACACCCTGG CCGGTACAGA 700
   GGTTTCTGCA CTGCTGGGTC GTATGCCATC GGCGGTAGGT TATCAGCCAA 750
60 CGCTGGCTGA AGAGATGGGT GTGCTGCAGG AGCGTATTAC CTCCACCAAG 800

```

ACCGGTTC

5 2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
 ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAAGTTCGC TGTATCGCAA 100
 TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
 AACCCAATTT CTGTTCCAGT GGGAAACGAAA ACATTGGGTC GTATCATGAA 200
 25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
 ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300
 ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
 TGCGAAAGGG GGTAAGTAG GTTTATTCGG TGGTGCGGGT GTCGGTAAAA 400
 CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
 30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
 CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550
 ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
 GGCTTAACTA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
 CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
 35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCCTTGCA 750
 GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800
 TATTA 805

40

2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
 CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCTG 100
 TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
 50 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCTG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTAAGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGGCGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAAACC	GGTTCAATCA	CTTCTGTA			828

15

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	GTTCAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGCACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
40	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTTGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GGTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
45	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTCGTC	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

50

2) INFORMATION FOR SEQ ID NO: 335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 811 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

```

10 CCCTAAAGTA TACGACGCTC TTGAGGTTAT GAATGGTAAA GAGAAACTGG      50
   TGCTAGAAGT TCAGCAACAG TTAGGCGGTG GTATCGTTCG TTGTATCGCA      100
   ATGGGTACAT CAGACGGTTT AAGCCGTGGC TTAAAAGTTG AAAACTTAGG      150
   CCACCCAATT GAAGTACCAG TAGGTAAAGC AACACTGGGA CGTATCATGA      200
   ACGTTCTGGG TACACCTATC GATATGAAAG GTGATATTGC AACTGAAGAA      250
   CGTTGGTCTA TTCACGCGA AGCGCCAACC TATGAAGAGT TATCAAGCTC      300
15  TCAAGAACTA CTAGAAACCG GTATCAAAGT AATGGACTTA ATCTGTCCGT      350
   TTGCTAAAGG TGGTAAAGTA GGTCTCTTCG GTGGTGCGGG TGTTGGTAAA      400
   ACAGTTAACA TGATGGAATT GATCCGTAAC ATCGCGATTG AGCACTCAGG      450
   TTATTCTGTA TTTGCAGGTG TTGGTGAGCG TACTCGTGAG GGTAACGACT      500
   TCTATCATGA AATGACAGAT TCTAACGTTT TTGACAAAGT ATCGTTAGTT      550
20  TATGGTCAGA TGAATGAGCC ACCAGGAAAC CGTCTACGTG TAGCACTGAC      600
   GGGTTTAACC ATGGCGGAAA AATTCCGTGA TGAAGGCCGT GACGTACTGT      650
   TATTCGTCGA TAACATCTAT CGTTACACCT TAGCCGGTAC CGAAGTATCA      700
   GCACTGTTAG GCCGTATGCC ATCAGCAGTA GGTTACCAAC CAACATTGGC      750
   TGAAGAGATG GGTGTTCTGC AAGAACGTAT CACTTCAACC AAAACAGGTT      800
25  CAATCACCTC T                                     811

```

2) INFORMATION FOR SEQ ID NO: 336

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

```

45  TCAAGATAAC GTACCAAAAAG TGTACGATGC TCTTGAGGTT ATTAACGGTA      50
   AAGAAAAACT GGTGTTGGAA GTTCAACAAC AGTTAGGTGG TGGTGTGTGC      100
   CGTTGTATCG CAATGGGTAC ATCAGATGGT CTGAGCCGTG GTTTAGAAGT      150
   TGTAAACTTA GAGCACCCAA TCGAAGTACC AGTCGGTAAA GCAACTCTGG      200
   GACGTATCAT GAACGTTCTG GGTGAACCAA TCGACATGAA AGGTGATATC      250
50  GGCGAAGAAG AGCGCTGGTC TATTACCGT GCTGCACCAA GCTACGAAGA      300
   ATTAGCTAAC TCAACTGAAC TGCTGGAAAC CGGTATCAAA GTAATGGACT      350
   TAATCTGTCC ATTCGCGAAA GGTGGTAAAG TAGGTCTGTT CGGTGGTGCG      400
   GGTGTTGGTA AAACCGTAAA CATGATGGAA CTGATCCGTA ACATCGCGAT      450
   TGAGCACTCA GGTTACTCAG TGTTGCTGAG TGTTGGTGAG CGTACCCGTG      500
55  AAGGTAACGA CTTCTATCAT GAAATGACAG ACTCAAACGT TCTGGATAAA      550
   GATCACTGGG TTTATGGCCA GATGAACGAG CCACCAGGAA ACCGTCTGCG      600
   TGTTGCGCTG ACTGGTCTGA CTATGGCTGA AAAATTCCGT GACGAAGGTC      650
   GTGACGTACT GCTGTTTCGT GACAACATTT ATCGTTATAC ACTGGCAGGT      700
   ACTGAAGTAT CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA      750
50  ACCAACGCTG GCGGAAGAGA TGGGTGTTCT TCAAGAACGT ATTACCTCAA      800

```

5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTAA 50
CGGTAAAGAA ACACTGGTGC TGGAAAGTTCA GCAACAGTTA GGCGGTGGTG 100
TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
GGACTTAATC TGTCCATTCG CGAAAGGTGG TAAAGTTGGT CTGTTCCGTG 400
GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAAGTATG CCGTAACATC 450
30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTTG GTGAGCGTAC 500
TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTAGG 700
35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

10 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
ACTGGTGTG GAAGTTCAGC AGCAGTTAGG CCGTGGTGTT GTCCGTGTGA 100
TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTTG	400
5	GTAAAACAGT	AAACATGATG	GAACTGATCC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTGCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAAG	TGTACGATGC	GCTTGAGGTT	GTAAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTTTCAGCAAC	AGTTAGGCGG	TGGTGTGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
10	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
15	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
	CTAAGACAGG	TTCTATCAC				819

50

2) INFORMATION FOR SEQ ID NO: 340

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 5 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

```

10 AACCGCACTG ACGTGCCTCA AATTTATGAC GCGTTAGTTG TAGATGGTAC      50
   CGAAACCACC CTAGAAGTTC AGCAGCAGCT GGGCGATGGT GTGGTACGTA      100
   CTATTGCAAT GGGATCTACT GAAGGTCTTA AGCGTGGTTT ACCAGTAACA      150
   AACACTGGTG CCCCAATTAC AGTTCCAGTA GGTGATGCGA CTTTAGGTCG      200
   TATTATGGAC GTTTTAGGTC GTCCAATTGA CGAACAAGGT CCAGTTAATT      250
   CTGAAGACCA TTGGTCAATC CACCGTCAAG CGCCATCATA TGATGAGCAA      300
15 GCTAACAGTA CTGACCTATT AGAGACAGGT ATTAAAGTAA TTGACTTACT      350
   TTGTCCGTTT GCTAAAGGGG GTAAAGTTGG TCTGTTCCGT GGTGCCGGTG      400
   TTGGTAAAC  CGTAAACATG ATGGAATTGA TTAATAACAT CGCTCTTAAG      450
   CACTCAGGTT TATCAGTATT CGCTGGTGTG GGTGAGCGTA CTCGTGAAGG      500
   TAACGACTTC TACCACGAGA TGCAAGAAGC GGGTGTGTTT GACGTTGAAA      550
20 ACTTCACCAA CTCAAAGTT  GCGATGGTTT ATGGTCAGAT GAATGAGCCA      600
   CCAGGTAACC GTTTACGTGT TGCCTTAACC GGTCTGACTA TGGCTGAGTA      650
   CTTCCGTGAT CAAAAAGATG AAAACGGTAA AGGTAAAGAC GTTCTATTAT      700
   TCGTTGATAA CATCTACCGC TACACGCTAG CCGGTACTGA AGTATCAGCA      750
   CTTCTAGGTC GTATGCCATC AGCAGTAGGT TATCAGCCAA CACTAGCGGA      800
25 AGAGATGGGT GTACTACAAG AGCGTATTAC TTCAACTCAG ACTGGTTCTA      850
   TTACTTC                                     907

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30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 40 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

```

45 GTTCCCTCAG GATGCAGTAC CGAACGTGTA CAATGCTCTT GAGGTAGAAA      50
   ACGGTACCTC CAAACTGGTG CTGGAAGTTC AGCAACAGTT AGGCGGCGGC      100
   GTTGTTCGTT GTATCGCAAT GGGTACCTCA GACGGCCTGC GTCGCGGTCT      150
   GAAAGTGAAC AACCTGGAAC ACCCAATTGA AGTACCGGTA GGTAAAGCGA      200
50 CTCTGGGTCG TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAAGGT      250
   GAAATCGGCG AAGAAGAACG TCGTGCTATT CACCGTGCTG CGCCTTCTTA      300
   TGAAGAGCTG GCAAATCCC AGGAATTGCT GGAAACCGGT ATCAAAGTTA      350
   TGGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCCGT      400
   GGTGCGGGTG TAGGTAAAAC TGTGAACATG ATGGAGCTGA TCCGTAACAT      450
55 TGCGATCGAG CACTCCGTTT ATTCTGTGTT TGCAGGCGTG GGTGAACGTA      500
   CTCGTGAGGG TAACGACTTC TACCACGAAA TGACTGATTC CAACGTTATC      550
   GACAAAGTTT CCCTGGTGTA TGGCCAGATG AATGAGCCAC CAGGTAACCG      600
   TCTGCGCGTT GCACTGACCG GCCTGACCAT GGCGGAAAAA TTCCGTGATG      650
   AAGGTCGTGA CGTACTGCTG TTCGTTGACA ACATTACCAG TTACACCCTG      700
60 GCCGGTACCG AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG      750

```

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 55 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCCA	CGCTGGGTCG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAACCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAGTTCGG	TCTGTTTCGGT	GGTGCGGGTG	400
	TAGGTAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCGTTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTA	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAG	ATCTCGAACA	CCCAGTCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCGGC	GCCGTCTTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGACAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

```

10 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC      200
15  GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCTGC GCCGTCCTAC      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG      400
   GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
20  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ATAAAGTATC CCTGGTGTAT GGTGAGTGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA      650
   AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
25  CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
   TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
   CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                      831

```

30 2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

```

   TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
50  GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC      200
   GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAT      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG      400
55  GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
   GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA      650
60  AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700

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CCGGTACGGA	AGTTTCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
TATCAGCCAA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
CTCCACCAA	ACCGGTTCTA	TCACCTCCG			829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
25	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
30	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
35	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
40	CGGTTCTATC	ACCTCCG				817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAGAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCTGAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTGCACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTGG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTAA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CGGTTC					806

20

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
 (B) STRAIN: ATCC 43972

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTGCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCTTAC	300
	GAAGAGTTGT	CAAACTCTCA	GGAAGTGTCT	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	400
45	GCGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTAAGTGTGT	TCGTGATATA	CATCTATCGT	TATACCTTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases

60

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACTCTCA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTAATGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACTCTCA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500

	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	561
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
5	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	CGCAGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Virchow

(B) STRAIN: ATCC 51955

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
30	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGG	GAACGTA	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTCTCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
40	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
45	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: ATCC 33105

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTT	GCCAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia fonticola*
 (B) STRAIN: ATCC 29844

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACCGA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCGTT	GCCAAGGGTG	GTAAAGTTGG	TCTGTTTCGGT	GGTGCTGGTG	400
	TAGGTAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTAAGT	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50
 TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100
 GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150
 GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAGCTA CTCTGGGCCG 200
 20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250
 AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300
 GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
 CTGCCCCGTT CGCAAGGGTG GTAAAGTCGG TCTGTTTCGT GGTGCGGGTG 400
 TTGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 25 CACTCCGGTT ATTCTGTGTT TCGGGGCGTG GGTGAGCGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGAACGACTC CAACGTA CTG GACAAAGTAT 550
 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
 GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
 30 AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
 ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCTACCAA 800
 GACTGGTTCA ATCACCTCCG TA 822

35

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG 50
 AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG 100
 TATCGCGATG GGGACCTCAG ATGGTCTGCG CGCGGTCTG AAAGTGAACG 150
 55 ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200
 ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA 250
 AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT 300
 CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350
 TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTTCGGTG GTGCTGGTGT 400
 60 TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

	ACTCCGGTTA	TTCCGTGTTT	GCAGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
5	GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
	AGTGTCCGCA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
	ACCGGTTCTA	TCACTTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia marcescens*

(B) STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

	TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
	CCGAAAAACT	GGTGTGGAA	GTTCAAGCAAC	AGCTGGGCGG	TGGCGTGGTT	100
30	CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
	GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
	GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
	GGCGAAGAAG	AGCGTTGGGC	GATTCACCGC	GCGGCGCCAA	GCTACGAAGA	300
	GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
35	TGATTTGTCC	GTTGCGCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
	GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
	CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
	AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
	GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
40	CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
	GTGACGTTCT	GCTGTTTCGT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
	ACCGAAGTGT	CCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
	GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
45	CCAAG					805

2) INFORMATION FOR SEQ ID NO: 358

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia odorifera*

60 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	AACTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTGGTTCGTT	100
	GTATCGCTAT	GGGCACCTCC	GACGGTTTGC	GTGCGGCCT	GAAAGTGAAC	150
	GATCTGCAAC	ACCCAATCGA	AGTCCCAGTT	GGCAAGGCAA	CGCTGGGTCG	200
	TATCATGAAC	GTATTGGGTC	AACCAATCGA	CATGAAAGGC	GACATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCAAGCTA	CGAAGAAGTG	300
10	TCCAACCTCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTTA	TGGACCTGAT	350
	CTGCCCCGTT	GCCAAGGGTG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGTG	400
	TTGGTAATAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCAGTGTT	TGCGGGCGTG	GGTGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTAAGT	GACAAGGTTT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CGGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCCGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCTGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 359

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: ATCC 183

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

40	GTGTACAACG	CTCTTGAGGT	AGAAAACGGT	GCCAATAAGC	TGGTGCTGGA	50
	AGTTCAGCAA	CAGCTGGGCG	GTGGCGTGTT	TCGCTGTATC	GCGATGGGGA	100
	CCTCTGATGG	TCTGCGTCGC	GGTCTGAAAG	TGATCGACCT	GGATCACCCG	150
	ATTGAAGTAC	CGGTAGGTAA	AGCTACCCGT	GGCCGTATCA	TGAACGTATT	200
	GGGTGAACCA	ATCGACATGA	AAGGCGACAT	CGGCGAAGAA	GAACGTTGGG	250
45	CAATTCACCG	TCCAGCGCCA	AGCTACGAAG	ATTTGGCCAA	CTCCCAGGAT	300
	CTGCTGGAAA	CCGGTATCAA	GGTTATGGAC	CTGATCTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTGGGTCTGT	TCGGCGGTGC	GGGCGTGGGT	AAAACCGTAA	400
	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAACACTC	CGGTTATTCC	450
	GTGTTTGCGG	GCGTGGGTGA	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
50	CGAAATGAAC	GACTCCAACG	TACTGGACAA	AGTATCCCTG	GTTTACGGCC	550
	AGATGAACGA	GCCACCGGGT	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCGG	AGAAATTCCG	TGACGAAGGC	CGCGACGTC	TGCTGTTCTG	650
	TGATAACATC	TACCGTTATA	CCCTGGCCGG	TACCGAAGTG	TCCGCACTTC	700
	TGGGCCGTAT	GCCATCTGCG	GTAGGTTATC	AGCCAACGCT	GGCGGAAGAG	750
55	ATGGGCGTTC	TGCAAGAACG	TATCACCTCT	ACCAAGACCG	GTTCTATCAC	800
	CTCCG					805

60 2) INFORMATION FOR SEQ ID NO: 360

215

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

15 TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA 50
 CGGTAACGAA AAACCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGCG 100
 TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
 AAAGTTAACG ACCTCGAGCA CCCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
 20 GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
 ACATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCAAGCTAC 300
 GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT 350
 GGACCTGATC TGCCCGTTCG CCAAGGGTGG TAAAGTTGGT CTGTTGCGTG 400
 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
 25 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
 ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
 30 CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
 CTCGACCAAG ACCGGTTCAA TCACCTCCGT A 831

35 2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCDC D7172

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

CCGTAAACAT GATGGAAGT ATCCGTAACA TCGCCATCGA GCACAGCGGT 50
 TATTCCGTGT TCGCCGGTGT GGTGTAGCGT ACTCGTGAGG GTAACGACTT 100
 CTACCAGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
 55 ACGGTGAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
 GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
 GTTCGTGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
 CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT 350
 GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC 400
 60 GATCAC 406

2) INFORMATION FOR SEQ ID NO: 362

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA	50
	TGGTAATGAG CGTCTGGTGC TGGAAATTCA GCAGCAGCTC GGCGGCGGTA	100
	TCGTGCGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG	150
	GATGTAAAAG ACCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC	200
	TCTGGGCCGT ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG	250
25	AGATCGGTGA AGAAGAGCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAC	300
	GAAGAGCTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT	350
	CGACCTGATG TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG	400
	GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC	450
	GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC	500
30	TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG	550
	ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT	600
	CTGCGCGTTG CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA	650
	AGGTCGTGAC GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG	700
	CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT	750
35	TATCAGCCGA CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC	800
	CTCCACCAAA ACTGGTTCTA TCACCTCCGT A	831

40 2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55

	GCCGTACCGC GCGTGTACGA TGCTCTTGCG GTGCAAAATG GTAATGAGCG	50
	TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA	100
	TCGCAATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAC	150
	CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT	200
60	CATGAACGTA CTGGGTGAAC CGGTGCACAT GAAAGGCGAG ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTA CTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAA AAC	800
	CG					802

15

2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
35	ACCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAAC TGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
40	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCCG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
45	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACTGGTTCTA	TCACCTCCG				819

50

2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

218

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

GTACCGCGCG TGTACGATGC TCTTGAGGTG CAAAATGGTA ATGAGCGTCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CCGTATCGTG CGTACCATCG 100
 10 CAATGGGTTC CTCCGACGGT CTGCGTCGCG GTCTGGATGT AAAAGACCTC 150
 GAACACCCGA TCGAAGTCCC GGTAGGTAAA GCGACTCTGG GCCGTATCAT 200
 GAACGTACTG GGTGAACCGG TCGACATGAA AGGCGAGATC GGTGAAGAAG 250
 AGCGTTGGGC GATTACCGC GCAGCACCTT CCTACGAAGA GCTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAAC CCGTATCAAA GTTATCGACC TGATGTGTCC 350
 15 GTTCGCTAAG GGCGGTAAAG TTGGTCTGTT CCGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTCATTCGTA ACATCGCGAT CGAGCACTCC 450
 GGTTACTCTG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGACAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCTCTG 600
 20 ACCGGTCTGA CCATGGCTGA GAAATTCCGT GACGAAGGTC GTGACGTTCT 650
 GCTGTTTCGTT GACAACATCT ATCGTTACAC CCTGGCCGGT ACGGAAGTAT 700
 CCGCACTGCT GGGCCGTATG CCTTCAGCGG TAGGTTATCA GCCGACCCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAAACTGG 800
 TT 802

25

2) INFORMATION FOR SEQ ID NO: 366

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

TAACGCCCTTG GTTATTGATG TGCCTAAAGA AGAAGGTACA ATACAACATAA 50
 CATTAGAAGT TGCCTGCAA TTAGGTGACG ACGTTGTTCG TACAATTGCG 100
 45 ATGGATTCAA CTGATGGTGT CCAAAGAGGC ATGGATGTAA AAGATACAGG 150
 CAAAGAAATT AGTGACCTG TTGGTGATGA AACATTAGGT CGTGTATTTA 200
 ATGTACTAGG TGAAACAATT GACCTTAAAG AAGAAATTAG TGATTCTGTT 250
 CGCCGCGATC CTATCCATCG TCAAGCACCA GCATTCGATG AACTTTCAAC 300
 AGAAGTTCAA ATTTTAGAAA CAGGTATTAA AGTAGTAGAT TTAGTAGCAC 350
 50 CTTATATTAA AGGTGGTAAA ATCGGATTGT TCGGTGGTGC CCGTGTAGGT 400
 AAAACAGTAT TAATCCAAGA ATTAATTAAC AACATCGCTC AAGAGCACGG 450
 TGGTATTCTT GTATTCGCCG GTGTAGGTGA ACGTACTCGT GAAGGTAACG 500
 ATTTATACTT CGAAATGAGT GATAGTGGTG TAATTAAGAA AACAGCCATG 550
 GTATTGCGGC AAATGAATGA GCCACCTGGT GCACGTATGC GTGTTGCATT 600
 55 ATCTGGTTTA ACAATGGCTG AATATTTCCG TGACGAACAA GGTCAAGACG 650
 TATTATTATT CATCGATAAC ATTTTCAGAT TTACACAAGC TGGTTCTGAG 700
 GTATCTGCAT TATTAGGTCG TATGCCTTCT GCAGTAGGTT ACCAACCAAC 750
 ACTTGCTACT GAAATGGGAC AATTACAAGA ACGTA 785

60

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50
 AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100
 20 GCGATGACGT TGTTGCTACC ATTGCAATGG ATTCAACTGA TGGTGTTAAA 150
 CGTGGTAAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG 200
 AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250
 TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCCTAT ACATAGAGAA 300
 GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350
 25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAGTTG 400
 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA 450
 ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTCACTCT TTGCCGGTGT 500
 AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550
 GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600
 30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAAACA TGGCTGAATA 650
 TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700
 TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA 750
 CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800
 ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 50 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50
 55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100
 ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150
 TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200
 GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250
 CGATTTAGAT GAAAAGATTG ATGATTCAGT ACGTCGTGAT CCTATTCATA 300
 60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTGG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTT	AGTATTCGCC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTGTCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTCG	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAACA	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAAGAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

- (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

5
AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50
AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100
CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150
GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTCTAG GAAGAGTGTT 200
10 TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTGAG 250
TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA 300
ACAAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350
ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400
GTAAAACCGT ACTAATCCAA GAACCTTATTA ATAACATCGC TCAAGAACAC 450
15 GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500
TGATCTTTAC TATGAAATGA GTGACAGTGG TGTTATCAAG AAAACTGCAA 550
TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600
TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA 650
TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700
20 AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750
ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787

25 2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

40
GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50
TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAACCTA GGTGATGACG 100
TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG 150
GAAGTTTCAGA AACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC 200
45 TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250
AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300
TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350
TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG 400
GTGGTGCCGG TGTTGGTAAA ACCGTTTTTAA TCCAAGAATT GATTAATAAT 450
50 ATCGCACAAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500
TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA 550
TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA 600
CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA 650
TGAACAAGGA CAAGACGTTT TGTTATTCAT CGATAACATT TTCAGATTTA 700
55 CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750
GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800
TATTACATCA ACGAATAAAG GTTCAGTAAC 830

60

2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
 CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT 100
 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150
 20 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCCTGTA 200
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
 TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400
 25 TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
 TAGTGCGCTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
 30 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTATTCA TTGACAATAT 700
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATT TTAGGACGTA 750
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
 TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846

35

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
 CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT 100
 55 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150
 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCCTGTA 200
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
 TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
 60 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400

TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
 TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
 5 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAAGT TTCAGCATTA TTAGGACGTA 750
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
 10 TTACAAGAAC GTATTACATC TACTAATAAA GGTTTCAGTCA CTTCAA 846

2) INFORMATION FOR SEQ ID NO: 374

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus lugdunensis*
 25 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

ATAATGAAGT GCCTGAAATA AATAATGCGC TCATTGTTGA AATTCCTAAA 50
 30 AGTGATACAA CAATCAGTTT AACACTTGAA GTTGCTTTGC AATTAGGTGA 100
 CGATGTTGTA CGTACTATTG CAATGGATTC AACTGATGGC GTTCAACGTG 150
 GTATGGAAGT TCAAAACACA GGTAAGACA TCAGTGTACC TGTGAGAT 200
 GAAACATTAG GAAGAGTATT TAACGTTTGA GGAGAATCTA TTGATTAGA 250
 AGAAAAGCTA GATGACTCTG TCGTAGAGA TCCAATTCAT AGACTAGCAC 300
 35 CTAAATTTGA TGAATTATCT ACAGAAGTAG AAATTCTTGA AACTGGTATT 350
 AAAGTTGTTG ATTTATTAGC ACCATATATT AAAGGTGGTA AAGTTGGATT 400
 GTTTGGTGGT GCCGGAGTAG GTAAAACGGT ATTAATTCAA GAATTAATCA 450
 ACAATATTGC TCAAGAACAT GGTGGTATTT CTGTGTTTGC CGGAGTAGGT 500
 GAACGTACAC GTGAAGGTAA TGACTTATAT TATGAAATGA GCGATAGTGG 550
 40 CGTAATTAAG AAAACAGCGA TGGTATTTGG CCAATGAAT GAACCACCTG 600
 GTGCACGTAT GAGAGTTGCG TTATCTGCCT TAACAATGGC TGAATATTTT 650
 CGTGACGAGC AAGGACAAGA CGTATTGCTG TTTATCGATA ATATATTCCG 700
 TTTTACACAA GCAGGTTTCA AAGTATCTGC ATTACTTGA CGTATGCCAT 750
 CTGCCGTTGG TTATCAACCA ACATTGGCTA CAGAAATGGG ACAATTGCAA 800
 45 GAAAGAATTA CATCTACAAA TAAAGGTTCT GTAAC 835

2) INFORMATION FOR SEQ ID NO: 375

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

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5  GAGCACAATG AAGTTCCAGA AATTAACAAT GCCTTAGTCG TAGACGTTGA      50
   AAGAGATGAA GGTACAGTAT CTCTTACATT AGAAGTGGCA TTACAACTTG      100
   GCGATGATGT CGTACGTACA ATTGCAATGG ATTCTACTGA TGGTGTAAAA      150
   CGTGGTACAG AAGTTTCGAGA TAGCGGAGAT AGCATCAGTG TTCCAGTTGG      200
   TGATGCTACG TTAGGACGTG TGTTTAATGT TCTTGGTGAT ACAATTGACT      250
10  TAGACGAGAA GCTTGATACT TCTGTCAAAC GTGATCCAAT TCATAGAGAA      300
   GCACCTGCAT TCGATCAATT ATCAACAAAA GTTGAAATCT TAGAAACAGG      350
   TATTAAAGTA ATTGATTTAC TTGCACCATA TATTAAAGGT GGTAAAATCG      400
   GTTTATTCGG TGGCGCTGGT GTAGGTAAAA CAGTATTAAT TCAAGAATTA      450
   ATTAATAATA TAGCTCAAGA ACATGGTGGT ATTTTCAGTAT TTGCCGGCGT      500
15  AGGTGAACGT ACGCGTGAAG GTAATGACTT ATACTACGAA ATGAGTGATA      550
   GTGGTGTTAT TAAGAAAACA GCTATGGTCT TCGGACAAAT GAATGAGCCA      600
   CCTGGTGCGC GTATGCGTGT TGCTTTATCA GGCTTAACAA TGGCTGAACA      650
   CTTCCGTGAT GTACAAGGAC AAGATGTTTT ACTATTTATT GATAACATAT      700
   TCAGATTTAC GCAAGCTGGT TCAGAAGTAT CAGCACTATT AGGTCGTATG      750
20  CCATCAGCCG TTGGTTATCA ACCTACCCTT GCTACTGAAA TGGGTCAATT      800
   ACAAGAACGT ATTACATCAA CAACTAAAGG ATCTGTAACG TC              842

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25 2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 842 bases
      (B) TYPE: Nucleic acid
30     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Staphylococcus simulans
      (B) STRAIN: ATCC 27848

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

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40  TGATGAACTG CCTAAGATTA ATAACGCATT AGTGCTAGAT GTACCTAAGA      50
   AAGATGGCAC GACTGAATCT CTTACATTAG AAGTAGCACT TGAATTAGGC      100
   GACGACGTAG TTAGAACTAT CGCCATGGAC TCTACAGACG GAATTAAACG      150
   TGGTGACGAC GTTAAAGACA CTGGTCGTCC AATCAGTGTA CCTGTCGGTG      200
45  AAGATACGTT AGGAAGAGTA TTTAACGTTT TAGGTGATCC AATCGATAAT      250
   GATGGACCGA TTTCTGAATC AGTTCCACGT GAACCAATTC ATAGACAACC      300
   ACCTAAATTT GATGAATTAT CAACAAAAGT TGAACACTT GAAACTGGTA      350
   TCAAAGTAGT AGACTTATTA GCACCATATA TCAAAGGTGG TAAAGTTGGT      400
   TTATTCGGTG GTGCCGGAGT AGGTAAAAC TATTAAATCC AAGAATTAAT      450
50  TAATAACATC GCTCAAGAAC ACGGCGGTAT TTCAGTATTC GCAGGTGTTG      500
   GTGAACGTAC ACGTGAAGGT AACGACTTGT ACTTCGAAAT GAGCGACAGT      550
   GGTGTTATCA AGAAAACAGC GATGGTATTC GGACAAATGA ACGAACCACC      600
   TGGTGCACGT ATGCGTGTAG CTTTATCAGG TTTAACAATG GCTGAATACT      650
   TCCGTGATGT TAAAGGACAA GACGTTCTTT TATTCATCGA TAACATTTTC      700
55  CGCTTCACAC AAGCAGGTTT TGAGGTATCA GCATTGCTTG GCCGTATGCC      750
   ATCAGCCGTT GGTTACCAAC CAACATTGGC AACAGAAATG GGTCAATTAC      800
   AAGAACGTAT CACTTCTACA ATGAAAGGTT CTATCACATC TA              842

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60

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG	TCCCTGATAT	TAATAATGCC	CTTATTATTG	AAGTTCCAAA	50
AGAAGATGGA	ACGTTAAACT	TAACATTAGA	AGTTGCACTA	CAATTAGGTG	100
ATGATGTTGT	ACGTACAATT	GCAATGGATT	CAACTGATGG	TGTTCAAAGA	150
GGCATGGATG	TTAAAGACAC	AGGTAAAGAT	ATTAGTGTAC	CTGTAGGCCA	200
TGAAACGCTT	GGAAGAGTGT	TTAATGTACT	AGGTGAAACA	ATTGACTTGG	250
AAGAGAAAAT	TGATGATTCC	GTACGTCGTG	ATCCAATCCA	TAGACAATCA	300
CCAGGTTTCG	ATGAATTATC	TACTGAAGTA	GAAATCTTAG	AAACAGGTAT	350
TAAAGTAGTA	GACTTATTAG	CACCTTACAT	TAAAGGTGGT	AAAGTTGGAC	400
TATTCGGTGG	TGCCGGAGTA	GGTAAACCG	TTTTAATCCA	AGAATTAATT	450
AACAATATTG	CACAAGAACA	TGGTGGTATT	TCAGTATTCG	CGGGTGTAGG	500
TGAACGTACT	CGTGAAGGTA	ATGATTTATA	CTATGAAATG	AGTGATAGTG	550
GTGTAATTAA	GAAAACAGCG	ATGGTATTTG	GACAAATGAA	TGAACCACCT	600
GGCGCACGTA	TGCGTGTAGC	TTTATCTGGT	TAACTATGG	CTGAATACTT	650
CCGTGATGAA	CAAGGACAAG	ACGTACTTTT	ATTCATCGAT	AATATTTTCA	700
GATTTACACA	AGCTGGTTCT	GAAGTTTCTG	CATTACTTGG	TCGTATGCCT	750
TCAGCCGTTG	GTTACCAACC	AACATTAGCA	ACTGAAATGG	GTCAATTACA	800
AGAACGAATT	ACATCTACAA	ATAAAGGTTT	TGTAACATCT	A	841

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA	ATGAACCGCT	TCCTGAGATA	AATAATGCAC	TTGTTGTTTA	50
CAAAGACAGT	GAGAAAAAAC	ATAAAATCGT	TCTTGAAGTA	GCTCTTGAAC	100
TTGGTGAAGG	CCTCGTTCGT	ACCATTGCTA	TGGAATCAAC	TGATGGTTTG	150
ACACGTGGTC	TAGAAGTTCT	TGATACAGGC	CGTGCAATCA	GTGTACCAGT	200
TGGTAAAGAA	ACGCTTGGAC	GTGTCTTCAA	CGTTCTTGGT	GATGCTATCG	250
ATCTTGAAGA	ACCATTTGGA	GAAGATGCAG	AACGTCACCC	CATTCATAAG	300
AGTGCCCCAA	CTTTTGATGA	ATTATCAACG	TCAACAGAAA	TCCTTGAAAC	350
AGGGATTAAA	GTTATCGACC	TACTTGCCCC	TTACTTAAAA	GGAGGGAAGG	400

TTGGACTTTT CGGTGGTGCC GGAGTTGGTA AGACCGTTCT TATCCAAGAG 450
 TTGATTCATA ACATTGCTCA AGAGCATGGT GGTATTTTCAG TATTTACCGG 500
 AGTTGGTGAA CGTACACGTG AAGGTAATGA CCTCTATTGG GAAATGAAAG 550
 AATCAGGCGT TATTGAAAAA ACAGCTATGG TATTTGGTCA GATGAATGAG 600
 5 CCACCTGGTG CACGTATGCG TGTAGCCCTT ACTGGTTTGA CAATCGCTGA 650
 ATATTTCCGT GATGTTGAAG GACAGGACGT GCTTCTCTTT ATTGATAACA 700
 TTTTTCGTTT CACACAAGCA GGTTCTGAAG TTTCAGCTCT TCTTGGACGT 750
 ATGCCATCAG CCGTTGGTTA TCAACCAACC TTGGCAACTG AAATGGGTCA 800
 ATTGCAAGAA CGTATCACGT CAACTAAAAA AGGTTCTGTT ACATCA 846
 10

2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus agalactiae*
 25 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 30 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTA CTCTTGAAGT 100
 TGGTGACGGC CTCGTTTCGT CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA 350
 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 40 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 45 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCAA 846

2) INFORMATION FOR SEQ ID NO: 380

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Streptococcus agalactiae*

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

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5  TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
   GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
10  TCTTGAAGAG CTTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC TTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAGG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
   TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
15  GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
   CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA      750
20  TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCAA      846

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25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Streptococcus agalactiae
(B) STRAIN: ATCC 12973

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

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40  TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GTGCAATTAG TGTGCCGGTT      200
45  GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
   CCTTGAAGAG CTTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC ATTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA      350
   GGTATTAAGG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
50  TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
   GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
55  CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA      750
   TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCA      845

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60

2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC 100
 TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 20 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CTTTTCGAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
 25 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 30 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845

35

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAC 100
 55 TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CTTTTCGAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
 60 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400

TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 5 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 10 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845

2) INFORMATION FOR SEQ ID NO: 384

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 25 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
 30 AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAAC 100
 TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCACTA 200
 GGTAAAGAAA CTTTGGGACG CGTCTTTAAT GTACTTGGAG AAACCATTTGA 250
 CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
 35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
 GGTATCAAGG TAATTGACCT TCTTGCCCCT TACCTTAAAG GTGGTAAAGT 400
 TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
 TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTCAGT ATTTACCGGT 500
 GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
 40 ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
 CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAC CATTGCTGAG 650
 TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
 CTTCCGTTTC ACTCAGGCAG GTTCAGAAGT ATCAGCCCTC TTAGGCCGTA 750
 TGCCTTCTGC TGTTGGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
 45 TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTTA CTTCT 845

2) INFORMATION FOR SEQ ID NO: 385

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

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5  TTGCGAGTGG GGACAAACTA CCAGAGATTA ATAATGCGTT GATAGTTTAT      50
   AAAGATGGCG ATAAAAAGCA AAAAATCGTT CTCGAGGTTG CCCTAGAGCT      100
   TGGAGACGGT ATGGTACGTA CAATTGCTAT GGAATCAACC GATGGGCTTA      150
   CACGTGGATT AGAGGTTCTT GATACTGGTC GTGCCATTAG TGTACCAGTT      200
   GGTAAGAGA CTCTAGGTCG TGTTTTCAAC GTTCTTGGTG AAACCATCGA      250
10  CCTAGAAGCA CCATTTCAG ATGATGTTAA TCGTGAACCG ATCCATAAAA      300
   AAGCACCAGC CTTTGATGAA TTGTCAACAT CATCAGAAAT TCTTGAAACA      350
   GGTATCAAGG TTATTGACCT GCTTGCCCCT TACTTAAAGG GTGGTAAGGT      400
   CGGTCTTTTC GGTGGTGCCG GAGTTGGTAA AACCGTTCTT ATCCAAGAAT      450
   TAATCCACAA TATCGCTCAA GAGCATGGTG GGATCTCGGT ATTTACCGGT      500
15  GTTGGTGAGC GTACGCGTGA AGGAAATGAC CTTTACTGGG AAATGAAGGA      550
   ATCAGGCGTT ATTGAAAAAA CAGCCATGGT TTTTGGTCAG ATGAATGAAC      600
   CACCAGGAGC CCGTATGCGT GTTGCCCTGA CCGGCTTGAC AATTGCTGAA      650
   TATTTCCCGC ATGTTGAAGG CCAAGACGTC CTGCTCTTCA TTGACAAATAT      700
   TTTCCGCTTT ACTCAAGCAG GCTCAGAGGT ATCAGCCCTT CTAGGTCGTA      750
20  TGCCTTCAGC CGTTGGTTAC CAGCCAACAC TTGCCACTGA AATGGGACAA      800
   TTGCAAGAGC GTATCACCTC AACGAAAAAA GGCTCTGTTA CCTCTA      846

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25 2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Streptococcus anginosus
(B) STRAIN: ATCC 27335

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

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40  TTGCAGCTGG TGATAAATTA CCTGAGATAA ATAATGCACT TGTAGTCTAT      50
   AAAAATGACG AAAATAAATC AAAAATCGTC CTTGAAGTAG CTCTTGAGCT      100
   TGGTGATGGA GTGGTTCGAA CTATTGCCAT GGAATCCACT GATGGGTTGA      150
   CTCGTGGCAT GGAAGTTCTA GATACTGGTC GACCAATTTT TGTTCAGTT      200
45  GGGAAAGAAA CACTTGGTCG CGTCTTTAAC GTTTTAGGCG ATACCATTGA      250
   TTTGGATACT CCATTGCGCG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCTCCAAC TTTTGATGAG TTATCTACTT CATCAGAAAT CTTAGAAACA      350
   GGAATAAAGG TTATTGACCT TTTAGCCCCC TACCTCAAAG GTGGGAAAGT      400
   CGGCCTCTTC GGTGGTGCTG GCGTTGGGAA AACTGTCTTG ATTCAAGAGT      450
50  TGATTCATAA TATCGCCCAA GAACACGGCG GGATTTCAGT CTTTACTGGT      500
   GTTGGGGAAC GAACTCGTGA AGGGAATGAC CTGTACTGGG AAATGAAAGA      550
   ATCTGGTGTT ATCGAAAAGA CGGCTATGGT CTTTGGGCAA ATGAATGAAC      600
   CGCCTGGAGC ACGTATGCGT GTAGCTTTGA CTGGGTAAAC GATTGCAGAG      650
   TATTTCCGTC ATGTGGAAGG TCAAGATGTT CTTTGTGTTA TTGATAATAT      700
55  TTTCCGTTTC ACTCAAGCTG GTTCTGAAGT GTCAGCCCTT CTTGGTCGTA      750
   TGCCATCAGC TGTTGGTTAC CAACCAACCT TGGCTACTGA AATGGGGCAA      800
   TTACAAGAAC GTATTACATC AACGAAAAAA GGTTCTGTTA CCTCAA      846

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2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

GCAGCTGGTG ATAAACTTCC TGAGATTAAAC AATGCATTGG TCGTTTATAC 50
 TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG 100
 GAGAAGGTGT GGTTCTGACC ATTGCCATGG AATCTACTGA TGGATTGACT 150
 20 CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG 200
 TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT 250
 TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA 300
 GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG 350
 GATTAAAGTT ATCGACTTGC TAGCCCCCTTA CCTTAAGGGT GGTAAGTTCG 400
 25 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG 450
 ATTCACAACA TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT 500
 TGGTGAACGT ACACGTGAAG GTAATGACCT TTAAGGGAA ATGAAAGAAT 550
 CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA 600
 CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA 650
 30 CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT 700
 TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG 750
 CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT 800
 GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT 843

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2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT 50
 AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAC 100
 55 TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA 150
 CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC 200
 GGTAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA 250
 CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA 300
 AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA 350
 60 GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT 400

TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT 450
 TGATTCACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA 500
 GTTGGCGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
 ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
 5 CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
 TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
 CTTCCGTTTC ACACAGGCTG GTTCAGAAAGT GTCTGCCCTC TTGGGTCGTA 750
 TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
 TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTTCGTGTA C 841
 10

2) INFORMATION FOR SEQ ID NO: 389

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus uberis*
 25 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
 30 AGGTAGCGAT AAAAAACAAA AGATTGTTCT TGAAGTTGCT TTGGAACCTG 100
 GGGACGGAAT GGTTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
 CGTGGATTAG AAGTTTTAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
 AAAAGAAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
 TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
 35 GCCCCAGCAT TTGATGAACT ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
 AATAAAAGTT ATTGACTTAT TAGCCCCCTA TCTCAAAGGT GGTAAGTTG 400
 GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTTAAT TCAAGAATTA 450
 ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTTCAGTAT TTACCGGTGT 500
 TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
 40 CTGGCGTTAT TGAAAAACA GCCATGGTAT TTGGACAAAT GAACGAACCA 600
 CCAGGAGCAC GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
 TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
 TCCGTTTCAC GCAAGCTGGT TCAGAAGTTT CAGCCCTATT GGGTCGTATG 750
 CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
 45 GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

2) INFORMATION FOR SEQ ID NO: 390

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

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5  TTCCCTCAGG ACGCTGTACC ACAGGTGTAC AACGCTCTTG AGGTTGAAAA      50
   TGGTGATACC CGTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG      100
   TCGTTCGTAC GATTGCAATG GGAACCTCTG ACGGCCTGAA ACGTGGCCTT      150
   AAGGTGACCG ATCTGCAAAA ACCGATTCAG GTACCGGTCTG GTAAAGCGAC      200
   GCTGGGCCGT ATCATGAACG TACTGGGTCA GCCAATCGAT ATGAAAGGCG      250
10  ACCTGAAGAA CGAAGATGGT AGCAATGTTG AGGTGAACTC TATTCACCGT      300
   GCAGCGCCAA GCTACGAAGA ACTGGCTAAC TCTACTGAGC TGCTGGAAAC      350
   GGGTATCAAG GTTATCGACC TGATCTGTCC GTTTGCAAAA GGCGGTAAAG      400
   TGGGTCTGTT CGGTGGTGCG GGTGTAGGTA AGACCGTCAA CATGATGGAA      450
   CTGATCCGTA ACATCGCTAT CGAGCACTCT GGTTACTCTG TATTTGCAGG      500
15  GGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGACCG      550
   AGTCTAACGT TCTGGATAAA GTTGCTCTGG TTTATGGCCA GATGAACGAG      600
   CCACCAGGAA ACCGTCTGCG CGTTGCGCTG ACCGGTCTGA CTATGGCTGA      650
   AAAATTCCGT GACGAAGGCC GTGACGTACT GCTGTTTCGT GATAACATCT      700
   ATCGTTATAC CCTGGCCCGT ACTGAAGTTT CAGCACTGCT GGGTCGTATG      750
20  CCTTCTGCGG TAGGTTATCA GCCAACACTG GCCGAAGAAA TGGGTGTTCT      800
   TCAGGAACGT ATCACGTCAA CAAAACCGG TTCAATCACT TCCGTA          896

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25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Trabulsiella guamensis
(B) STRAIN: ATCC 49490

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

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40  TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTTATGAA      50
   TGGTAGTGAG CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GGTGGTGGTA      100
   TCGTACGTAC TATCGCCATG GGTCTTCCG ACGGTCTGCG TCGTGGTCTG      150
   GATGTAAAAG ATCTCGAGCA TCCGATCGAA GTCCCGGTAG GTAAAGCAAC      200
45  GCTGGGTCGT ATCATGAACG TGCTGGGTCA GCCGATCGAT ATGAAAGGCG      250
   ACATCGGCCG AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCGTCCTAC      300
   GAAGAGCTGT CCAGCTCTCA GGAAGTGTG GAAACCGGCA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
   GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTGAT TCGTAACATC      450
50  GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTCTGG      550
   ACAAAGTATC CCTGGTGTAT GGACAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CACTGACCGG TCTGACCATG GCTGAGAAGT TCCGTGACGA      650
   AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTACCGT TACACCTTGG      700
55  CGGGTACTGA AGTATCTGCA TCGTGGGCC GTATGCCTTC AGCGGTAGGT      750
   TACCAGCCGA CCCTGGCGGA AGAGATGGGT GTTCTTCAGG AACGTATCAC      800
   CTCAACCAAA ACCGGTTCTA TCACCTCCG          829

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60

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG 50
 AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT 100
 GGTGTTGTTC GTTGATATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG 150
 20 GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT 200
 CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA 250
 GGTCTATATG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC 300
 TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG 350
 TAATGGATCT GATTTGTCCG TTCGCTAAGG GCGGTAAAGT CGGTCTGTTC 400
 25 GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA 450
 TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT 550
 CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA 600
 CCGTCTGCGC GTTGCACTGA CCGGCTTGAC CATGGCGGAG AAATTCCGTG 650
 30 ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC 700
 CTGGCCGGTA CAGAGGTATC TGCCTGCTA GGTCGTATGC CATCAGCGGT 750
 AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA 800
 TCACCTCCAC CAAGACGGGT TCAATCACCT CCGTA 835

35

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

GCTGTACCAA AAGTGACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA 50
 GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CGGTGGTGTT GTTCGTTGTA 100
 55 TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTGAA AGTCATCAAC 150
 CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT 200
 CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG 250
 AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC 300
 AGCTCGCAAG ACTTGTTAGA AACCGGTATC AAGGTAATGG ACTTGATTG 350
 60 TCCGTTGCTT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400

235

GTAAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC 450
 TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
 TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
 5 CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
 ATTGCTGTTT ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
 TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
 CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACCAAGAC 800
 GGGTTCAATC AC 812
 10

2) INFORMATION FOR SEQ ID NO: 394

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia frederiksenii*
 25 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

AAAGTGTACA ACGCCCTTGA GGTTGAAGGT ACTGCTGAGA AGTTAGTACT 50
 30 GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
 GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
 CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
 ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
 GGGCAATCCA CCGCGAAGCG CTTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
 35 GATCTGTTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTCGC 350
 TAAAGGCGGT AAAGTCGGTC TGTTCCGGTG TGCGGGTGTA GGTAACCGG 400
 TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
 TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
 CCACGAGATG ACTGACTCCA ACGTTCTGGA CAAAGTATCC TTGGTTTATG 550
 40 GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
 CTGACCATGG CGGAGAAATT CCGTGATGAA GGTCGTGACG TATTGCTGTT 650
 CATCGATAAC ATCTATCGTT ATACCTTGGC CGGTACGGAA GTATCCGCAC 700
 TGCTGGGTCG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
 GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
 45 CA 802

2) INFORMATION FOR SEQ ID NO: 395

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

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5  GCTGTACCAA GAGTGTACAA CGCCCTTGAG GTTGAAGGCA CTGCTGAGAA      50
   GCTGGTGCTG GAAGTTCAGC AACAGCTAGG CCGTGGTGTT GTTCGTTGTA      100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GCGGGTTGAA AGTCATCAAC      150
   CTGGAACACC CAATTGAAGT GCCGGTTGGT AAATCAACTC TGGGCCGTAT      200
   CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
10  AAGAGCGTTG GGCAATCCAC CGCGAAGCGC CTTCTTACGA AGAGCTTGCC      300
   AGCTCACAAG ATTTGTTAGA AACC GGTTATC AAAGTAATGG ACTTGATTTG      350
   CCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAAACAGT AAACATGATG GAGCTTATTC GTAACATCGC GATTGAGCAC      450
   TCAGGTTATT CTGTATTTGC TGGTGTGGGT GAGCGTACTC GTGAGGGTAA      500
15  CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT      550
   TGGTGTATGG CCAGATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA      600
   CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
   ACTGTTGTTT ATCGATAACA TCTATCGCTA TACCTTGGCC GGTACGGAAG      700
   TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACG      750
20  CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACGT CCACCAAGAC      800
   GGGTTC

```

25 2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 806 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Yersinia pseudotuberculosis
   (B) STRAIN: ATCC 29833

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

```

40  GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTAGAAGGCA CAACTGAAAA      50
   GTTAGTGCTG GAAGTTCAGC AACAGTTGGG CCGTGGTGTT GTTCGTTGTA      100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTAACCAAC      150
   CTGGAACACC CGATCGAAGT ACCGGTTGGT AAAGCGACCC TTGGCCGTAT      200
45  CATGAACGTA TTGGGTGAAC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
   AAGAGCGTTG GGCAATCCAT CGCGAAGCGC CTTCTTATGA AGAGCTTGCT      300
   AGCTCACAAG ATCTGTTAGA AACC GGTTATC AAGGTTATGG ACCTGATTTG      350
   TCCGTTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
50  TCTGGGTATT CTGTATTTGC CCGTGTAGGT GAGCGTACCC GTGAGGGTAA      500
   TGACTTCTAC CATGAAATGA CTGACTCCAA CGTTTTGGAC AAAGTATCCT      550
   TGGTTTACGG CCAGATGAAT GAGCCACCAG GTAACCGTCT ACGCGTTGCA      600
   CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
   ACTGCTGTTT ATCGATAATA TCTATCGTTA TACCCTAGCT GGTACGGAAG      700
55  TATCCGCATG GCTGGGTCGT ATGCCATCAG CGGTAGGTTA TCAGCCAACA      750
   CTGGCTGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACTAAGAC      800
   GGGTTC

```

60

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

```

TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG      50
TGCAGCTGAG AAGCTTGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG      100
TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG      150
20 AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC      200
TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC      250
CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC      300
GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT      350
GGATCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
25 GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC      450
GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC      500
TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG      550
ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT      600
CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA      650
30 AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG      700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC      750
TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC      800
TTCCAATAAG ACGGGTTCAA TCACCTCCG      829

```

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

```

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG      50
AAACTGGTGC TGGAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC      100
55 TATCGCCATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG      150
ACCTCGAGCA CCCGATCGAA GTCCCAGTAG GTAAAGCAAC CCTGGGCCGT      200
ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA      250
AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT      300
CCAGCTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTAAT GGATCTGATC      350
60 TGCCCGTTCT CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT      400

```

	AGGTAAAACT	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	GCGATTGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGATC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
5	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTGATAA	CATCTACCGT	TATACCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAAA	800
10	ACCGGTTCTA	TCACCTCCG				819

2) INFORMATION FOR SEQ ID NO: 399

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*
 25 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
30	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATT	CATCAAGAAC	ATGATTACCG	GTACTTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
35	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCCTCC	550
40	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGCTCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
45	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
50	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTGCGCCG	TCCGAGA	1097

2) INFORMATION FOR SEQ ID NO: 400

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

```

10 CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT 50
   GGAAGTTTCA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCCTGGC 100
   CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG 150
   CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT 200
   CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT 250
15 GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC 300
   TGAGGCCCGT TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA 350
   AGATTGGTTT CAACCCCAAG TCCGTTCCCTT TCGTCCCTAT CTCTGGCTGG 400
   AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAAGGG 450
   ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG 500
20 AAGCCATTGA CAACATTGAT CCCCTGTTC GTCTTCCGA CAAGCCCCTT 550
   CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC 600
   TGTCCGTCGT GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTACCT 650
   TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC 700
   GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGT TCAACGTCAA 750
25 GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA 800
   AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC 850
   TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGATTG 900
   CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG 950
   ATYGTCTGTT CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC 1000
30 TTAATCTYTG GATTTTGCCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT 1050
   ACTTTTGTAT CATTGTCTAA TCCAAACCTT TTCCATTTYA TTGAAAACAG 1100
   GTAAGAAGTT GGAAGACTCC CCAAGTTTCG TCAAGWSYGG TGACTCTGCT 1150
   ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TCGGTTGAAG CCTACACTGA 1200
   ATATCCTCCT CTTGGTCTGT TCGCTGTCCG TGA 1233
35

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2) INFORMATION FOR SEQ ID NO: 401

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

```

   CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT 50
55 GGAAGTTTCA GACTCCCAAG GTTAGTACCC CTCTGCCCTAC TACATCAAGT 100
   TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC 150
   GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA 200
   GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC 300
60 ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC 350

```

	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAAC T'	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCCACA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCCCT	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCC TTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCCG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCGTCGGT	CGTGTCGAGA	CTGGTGTCAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCTTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCCA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
 TTTTTCGCTG CAAGTTCTCT ATAGCTAACA TGA 1283

5

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1103 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: DAL95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
 GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
 ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
 25 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
 CCTCATCATT GCCTCCGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
 ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
 CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
 TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
 30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450
 GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA 500
 GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
 TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
 CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG 650
 35 CCGTGTCGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700
 CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
 CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTTCAACG TCAAGAACGT 800
 TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
 ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
 40 CACCCCGGTC AGGTGCGCGC TGGTTACGCC CCCGTCCCTG ACTGCCACAC 950
 TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
 GTACCGGCAA GTCTGTTGAG AACAACCCA AGTTCATCAA GTCCGGTGAT 1050
 GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
 CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
5	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAGTACC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTGCGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCCGG	ATGGTCTGTA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGTGCGCT	CCTTCAACGC	CCAGGTCATC	900
	GTCTTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCTCTGA	950
	CTGCCACACT	GCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

30 2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 1151 bases |
| | (B) | TYPE: Nucleic acid |
| 35 | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- | | | |
|--|-----|------------------------------------|
| | (A) | ORGANISM: <i>Aspergillus niger</i> |
| | (B) | STRAIN: ATCC 9508 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGTTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	ACCGTTACA	ACGAATCGT	TAAGGAGACC	TCCAACCTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATTGCCCCCT	GGTATGGTCG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

CACCACCAGC AGCTCAAGGA AGGTGTCCCC GGTGACAACG TTGGTTTCAA 800
 CGTCAAGAAC GTTTCGTCA AGGAGGTTTCG CCGTGGAAC GTTGCCGGTG 850
 ACTCCAAGAA CGACCCCCCT CTTGGCTGTG AGAGCTTCAC CGCCCAGGTC 900
 ATCGTCTCA ACCACCCCGG TCAGGTCGGC GCTGGTTACG CTCCCGTCCT 950
 5 GGACTGCCAC ACTGCTCACA TTGCTTGCAA GTTCGCTGAG CTCCTTGAGA 1000
 AGATTGACCG CCGTACCGGA AAGTCTGTTG AATCTTCCCC CAAGTTCATC 1050
 AAGTCCGGTG ACGCTGCCAT CGTCAAGATG ATTCCCTCCA AGCCCATGTG 1100
 TGTTGAGGCT TTTACTGACT ACCCCCCTCT TGGTCGTTTC GCCGTCCGCG 1150
 A 1151

10

2) INFORMATION FOR SEQ ID NO: 406

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

GCTTAAAGCT GAACGTGAAC GTGGTATCAC CATTGATATC GCTCTCTGGA 50
 30 AGTTCGAAAC TCCTAAGTAC TACGTTACTG TTATTGATGC TCCAGGTCAC 100
 CGTGATTTCA TCAAGAACAT GATTACTGGT ACTTCCCAAG CCGATTGCGC 150
 CATTCTTATC ATTGCTGCCG GTGTCGGTGA ATTCGAAGCT GGTATCTCCA 200
 AGGAAGGTCA AACAGAGAA CACGCTCTTC TCGCTTTCAC CCTTGGTGTC 250
 AGACAACCTA TCATTGCCAT CAACAAGATG GACTCTGTCA AGTGGGACCA 300
 35 AAAGAGATAC GAAGAAATCG TCAAGGAGGC TTCCAACCTC GTCAAGAAGG 350
 TTGGTTACAA CCCCAGTCT GTTCCATTCG TTCCTATCTC TGGTTGGAAC 400
 GGTGACAACA TGTTGGAACC TACCACCAAC GCCCCATGGT ACAAGGGATG 450
 GACCAAGGAA ACCAAGGCTG GTGCCACTAA GGGTATGACT CTTATTGAAG 500
 CCATTGACGC CATTGAACCA CCAGTAAGAC CATCCGACAA GCCACTCCGT 550
 40 CTCCCACTCC AAGATGTTTA CAAGATTGGT GGTATCGGAA CTGTGCCAGT 600
 CGGCCGTGTC GAAACCGGTA TCATCAAGGC CCGTATGGTC GTTACCTTTG 650
 CTCCACCAAT GGTCACAACT GAAGTTAAGT CCGTTGAAAT GCACCACGAA 700
 CAACTTGCTC AAGGTAACCC AGGTGACAAC GTTGGTTTCA ACGTCAAGAA 750
 CGTTTCCGTT AAGGAAATCA GACGTGGTAA CGTCTGTGGT GACTCCAAGA 800
 45 ACGATCCACC AAAGGGCTGC GAATCTTTCA ACGCTCAAGT TATCGTCTTG 850
 AACCACCCTG GTCAAATCTC TGCTGGTTAC TCTCCAGTTC TCGATTGCCA 900
 CACTGCCCAC ATTGCCTGCA GATTGACGCA ACTCCTTGAA AAGATCGACC 950
 GTCGTTCTGG TAAGAAGATT GAAGACTCTC CAAAGTTTGT CAAGTCTGGT 1000
 GATGCCGCTA TCGTCAAGAT GATCCCAACC AAGCCAATGT GCGTTGAAAC 1050
 50 CTTCACTGAA TACCCACCAC TTGGTCGTTT CGCCGTCCGT GAT 1093

2) INFORMATION FOR SEQ ID NO: 407

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

```

10 CTTGGACAAA TTGAAGGCTG AAAGAGAAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCA TCAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
15 TTGGGTGTCA AACAATTGAT TGTGCTGTC AACAAGATGG ACTCTGTCAA      300
   ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAATCTCT      350
   TCAAGAAGGT TGGTTACAAC CCAAGACTG TTCCATTYGT TCCAATCTCT      400
   GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAAGTTACT GGTAAGACCT      500
20 TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAATGGTAT CATCAAAGCC GGTATGGTTG      650
   TTACTTTTCGC CCCAGCTGGT GTTACCACAT AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
25 CGTTAAGAAC GTTTCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
   GGATTGTCAC ACTGCCCACA TTGCTTGTA ATTCGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGT      1000
30 AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG      1050
   TGTGGAAGCT TTTACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG      1100
   A                                                                1101

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35

2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

```

   GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
   TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA      100
   GATTTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT      150
55 TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGCT ATTTCTAAGG      200
   ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGGTGTCAAA      250
   CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA      300
   CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG      350
   GTTACAACCC AAAGACTGTT CCATTCGTTT CAATCTCTGG TTGGAATGGT      400
60 GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA      450

```

	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTTGTGAC	TCTTTCAATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTTCG	TGTCAGAGA		1089

15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
50	ATTGTTTTGA	ACCATCCAGG	TCAAACTCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

60

2) INFORMATION FOR SEQ ID NO: 410

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

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15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CAAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTG  AAGAAATCAT CAAGGAAACC TCCAAC TTCG      350
    TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT      400
    GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
    TTACTTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
    ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCCACA TTGCTTGTA  ATTCTGACT TGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGTC      1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG      1050
    TGTTGAAGCT TCACTGACT  ACCCACCATT AGGTAGATTC GCTGTCAGAG      1100
    AT

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2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

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60  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CAAAATACC  ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200

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	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

2) INFORMATION FOR SEQ ID NO: 412

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1101 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - 35 (B) STRAIN: NCPF 3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCAC'TTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGCTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

5 2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
 (B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
 TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
 GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
 CTGTGCTATC TTGATCATTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA 200
 25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTTGGC CTACACCTTG 250
 GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
 GGACAAGAAC AGATTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
 AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
 TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
 30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
 TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
 TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
 GCCCCGTCGGC CGTGTCGAGA CCGGTGTCAAT CAAGCCCGGT ATGGTCGTCA 650
 CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
 35 CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCACCGT 750
 CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAACGTC TGCGGTGACT 800
 CCAAGAACGA CCCCCCATG GGTTGCTCTT CTTTCAACGC CCAGGTTATC 850
 GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900
 CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
 40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
 TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
 TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCCGC GTCAGAGA 1098

45

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

249

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

2) INFORMATION FOR SEQ ID NO: 415

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1102 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - (B) STRAIN: CBS 7987
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
45	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850

	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
5	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1094 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida famata</i>
	(B)	STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25	AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
	AAATTCGAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
	CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
	CTATTTTTRAT	TATTGCTGGT	GGTGTGCGTG	AATTGCAAGC	CGGTATCTCT	200
30	AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
	TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
	AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
	GTTGGTTACA	ACCCTAAGAC	TGTTCTTTTC	GTGCCAATTT	CTGGATGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
35	GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
	GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
	ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
	TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTCACTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
40	ACAATTAGCT	GAAGGTGTTT	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
	AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
	GAACCACCCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
	ACACCGCCCA	CATTGCTTGT	AAATTCGATG	CTTTACTCGA	AAAGATTGAC	950
45	AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTCG	TCAAGTCCGG	1000
	TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
	CTTTCATGA	ATACCCACCA	TTAGGTAGAT	TCGCTGTTAG	AGAT	1094

50

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1101 bases
55	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

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TTTGGACAAG TTGAAGGCTG AAAGAGAAAAG AGGTATCACT ATCGATATCG      50
CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT      100
CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC      150
10 TGACTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG      200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTCACC      250
CTAGGTGTTA GACAATTGAT TGTYGCTGTC AACAAGATGG ACTCTGTCAA      300
GTGGGATGAA TCCAGATTCTG CTGAAATCGT TAAGGAAACC TCCAACTTCA      350
TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCTG CCAATCTCT      400
15 GGTTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTGGTA      450
CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT      500
TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG      550
CCATTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC      600
GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG      650
20 TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA      750
CGTTAAGAAC GTTTCGGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG      800
ACTCCAAGAA GACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC      850
ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTTTT      900
25 GGACTGTCAC ACCGCCACA TTGCTTGTA GTTTGAAGAA TTGTTGAAA      950
AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG      1000
AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG      1050
TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG      1100
A
1101

```

2) INFORMATION FOR SEQ ID NO: 418

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 45 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

```

AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC      50
50 AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTACACAGA GATTTTCATCA      100
AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT      150
GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC      200
CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG      250
TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYGAG      300
55 GAAATCATCA AGGAAACCTC TAACCTTCGT AAGAAGGTTG GTTACAACCC      350
TAAGACTGTG CCATTCTGTT CTATCTCTGG ATGGAAYGGT GACAACATGA      400
TTGAGGCTTC TACCAACTGT CTTTGGTACA AGGGATGGGA GAAGGAGACC      450
AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT      500
TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG      550
60 ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA      600

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	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTGG	ACTGTCACAC	CGCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTGG	GAAGATTCGC	CGTCAGAGAC			1080

2) INFORMATION FOR SEQ ID NO: 419

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAACTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
	CCAGTTTGG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

2) INFORMATION FOR SEQ ID NO: 420

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*

60

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

5	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAGTATC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
	AGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATTTCCAA	GGATGGTCAA	ACTAGAGAAC	ACGCTTTATT	AGCATTCACT	250
10	TTAGGTGTTA	AGCAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCTGTATA	300
	GTGGGATGAA	AAGAGATTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTTCTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTCAAG	GGTAAGACCT	500
15	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGATAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTAT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCG	CCATCTGGT	GTTACCACTG	AAGTCAAAGT	CGTTGAAATG	700
	CACCATGAAC	AATTAGAAGA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
20	CGTCAAGAAC	GTCTCTGTTA	AGGATATCAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	TGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTCT	GCTGGTTACT	CTCCAGTTTT	900
	AGATTGTGAC	ACTGCCCACA	TTGCATGTAA	ATTCGATGAA	TTAATTGAAA	950
	AGATTGACAG	AAGAAGCTGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
25	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	AT					1102

30

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 1099 bases |
| 35 | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|--------------------------------|
| | (A) | ORGANISM: <i>Candida kefyr</i> |
| | (B) | STRAIN: ATCC 28838 |

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

	TGGACAAGTT	AAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	CGATATCGCT	50
	TTGTGGAAGT	TCGAAACTCC	AAAGTACCAA	GTTACCGTTA	TCGATGCTCC	100
	AGGTCACAGA	GATTTTCATCA	AGAACATGAT	TACTGGTACT	TCTCAAGCTG	150
50	ACTGTGCTAT	CTTGATTATT	GCTGGTGGTG	TCGGTGAATT	CGAAGCCGGT	200
	ATCTCCAAGG	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACCTT	250
	GGGTGTTAGA	CAATTGATTG	TTGCTATCAA	CAAGATGGAC	TCTGTTAAGT	300
	GGGATGAATC	TCGTTACCAA	GAAATTGTTA	AGGAAACCTC	CAACTTCATC	350
	AAGAAGGTCG	GTTACAACCC	AAAGAATGTT	CCATTCGTCC	CAATCTCTGG	400
55	TTGGAACGGT	GACAACATGA	TTGAAGCCAC	CACCAACGCT	CCATGGTACA	450
	AGGGTTGGGA	AAAGGAAACC	AAGGCTGGTA	CCGTCAAGGG	TAAGACCTTG	500
	TTGGAAGCTA	TTGACGCTAT	CGAACCACCA	ACCAGACCAA	CTGACAAGCC	550
	ATTGAGATTG	CCATTGCAAG	ATGTCTACAA	GATCGGTGGT	ATTGGTACTG	600
	TGCCAGTCGG	TAGAGTCGAA	ACCGGTGTCA	TCAAGCCAGG	TATGGTTGTT	650
60	ACCTTCGCCC	CAGCCGGTGT	CACTACCGAA	GTAAAGTCCG	TCGAAATGCA	700

	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	900
5	ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
	AACGACAGAA	GATCCGCTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1095 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
30	ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCCGT	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
35	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCAT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
40	GTCCGGTAGAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCACTTT	650
	TGCTCCAGCA	GGTGTACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
45	TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
50	GCTTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1104 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida lambica*
(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

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10 CTTGGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCTCAAGC      150
   AGATTGTGCT ATTTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
   GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT      250
   CTTGGTGTTA GACAATTGAT TGTTGCTATC AACAAGATGG ACTCTGTCAA      300
15 GTGGGACGAA TCCAGATTCG ATGAAATTTG TAAGGAAACC GCWAACTTCA      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT      400
   GGTTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA      450
   CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA      500
   CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC      550
20 AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG      600
   TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA      650
   TTGTCGTTTT CGTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA      700
   ATGCACCATG AACCAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT      750
   CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG      800
25 GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA      850
   GTCATTGTTT TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT      900
   TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG      950
   AAAAGATTGA CAGAAGAACC GGTAAGGCTA CTGAAGACCA TCCAAAGTCT      1000
   GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT      1050
30 GTGTGTYGAA GCTTTCACTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA      1100
   GAGA                                     1104

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35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

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50 GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT      50
   TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA      100
   GGTACACAGAG ATTTTCATCA GAACATGATC ACTGGTACTT CCCAAGCTGA      150
   CTGTGCTATC TTGATTATCG CTGGTGGTGT CCGTGAGTTC GAAGCCGGTA      200
55 TCTCTAAGGA CGGTCAAACC AGAGAGCACG CTTTGTGGC TTACACCTTG      250
   GGTGTCAAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG      300
   GGACCAATCT AGATTCGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA      350
   AGAAGGTTGG TTACAACCTT AAGACTGTTT CATTCTGTCG AATCTCTGGT      400
   TGGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA      450
60 GGGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT      500

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	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAGCCAA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTCTAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACCTG	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTTGG	TAGATTCGCT	GTCAGAGA	1098

15

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCCACC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTG	AAGAAATTGT	CAAGGAAACC	CAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAAT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTAAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTGTGT	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCTTGG	TCAAATTTCT	GCAGGTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	GTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTG	GCAGTCAGAG	1100
	A					1101

55

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

257

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
15	GGAAATTCTGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCGA	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTCGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTC AAG	TGGTCTC AGT	CTCGTTT CGA	GGAGATC GTC	AAGGAGG TTT	50
	CCAAC T TCA T	CAAGA AGG TT	GGTTACA AGC	CCGATG AGGT	TCCTT TCG TC	100
	CCCAT CTCTG	GCTGGA ACGG	CGACA ACATG	CTTGAG CCCCT	CCACCA ACTG	150
	CCCCT GGTAC	AAGGG ATGGA	CCAAGA AGAC	CAAGA AGGGT	GAGGTCA AGG	200
	GTAAG ACTCT	TCTCG AGGCC	ATTGAC GCCA	TCGAG CCCCC	CTCCCG TCCT	250
60	ACCGACA AGC	CCCTCC GCTT	GCCTCT TCAG	GATGTCT ACA	AGATCGG CGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCC	350
	GCATGGTCGT	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTC	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTT	GACTGCCACA	CCGCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

2) INFORMATION FOR SEQ ID NO: 428

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTGCGTG	AATTGGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCCGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAACTT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATCCAGA	CCAAC TGACA	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCTGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	ACACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

55 2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

10
 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG 50
 GAAATTTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100
 ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT 150
 GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTT 200
 15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG 250
 TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC 300
 AAAACACAGT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA 350
 GGTTGGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA 400
 ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT 450
 20 TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTGTTGA 500
 AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA 550
 GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600
 GTCGGTAGAG TTGAAACTGG TGTCATCAA GCGGTATGG TTGTTACTTT 650
 CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG 700
 25 AACCAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750
 AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA 800
 GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT 850
 TGAACCAACC AGGTCAAATC TCTGCTGTT ACTCTCCAGT CTTGGATTGT 900
 CACACTGCTC ATATTGCTTG TAAATTGCG ACCTTGTTG AAAAGATTGA 950
 30 CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG 1000
 GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA 1050
 GCTTTCACTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA 1094

35

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT 50
 GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT 100
 CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG 150
 55 TGCTATTCTT ATCATTGCCG GTGGTGTTGG TGAGTTCGAG GCTGGTATCT 200
 CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT 250
 GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA 300
 CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA 350
 AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG 400
 60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG 450

	TTGGGAGAAG	GAGACCAAGG	CTGGTGTGTG	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTTC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AACTGCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTGCC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCACT	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 261

(A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTCGAGACC	CCCAAGTACC	50
15	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTGAGGCTG	GTATCTCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCAC TACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCC	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCGG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCACA	TTGCTTG CAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCACTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCTGGTC	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTTCATCA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

2) INFORMATION FOR SEQ ID NO: 434

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Cryptococcus albidus*
- (B) STRAIN: ATCC 66030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTG	50
	GAAGTTCGAG	ACCCCCAAGT	ACAATGTCAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCCG	ACAAGCCCTT	600
	GCGATTGCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTCGGTCG	AGTCGAGACC	GGTGTATCA	AGGCTGGTAT	GGTCGTCACC	700
	TTGCCCCCTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TTCAACGCTC	AGGTCATTGT	900
	CTTGAACCAC	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTCTG	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTGCGCGT	CCGAGA	1146

55

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
- (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTTCATCGA	CGCCCCTGGT	100
CATCGTGACT	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15 CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTTCGAA	GCCGGTATCT	200
CCAAGGATGG	TCAGACTCGT	GAGCAGCTC	TGCTCGCCTA	CACCCTGGGT	250
GTCAAGCAGC	TCATTGTTCG	CATCAACAAG	ATGGACACCA	CCAAGTGGTC	300
CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
AGGTCGGCTA	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	400
20 AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCCT	GGTACAAGGG	450
CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
AGGCCATCGA	CGCCATCGAC	CCCCCACTC	GTCCCACCGA	CAAGCCTCTC	550
CGTCTTCCTC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
CGTCGGTCGT	GTTGAGACTG	GTGTTCATCA	GGCCGGTATG	GTCGTTACCT	650
25 TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
GAACAACCTCG	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
GAACGTCTCC	GTCAAGGAGG	TTCGTCGTGG	AAACGTCTGC	GGTGACTCCA	800
AGAACGACCC	ACCCAAGGGT	GCTGATTCTT	TCAACGCCCC	GGTCATCGTC	850
TTGAACCACC	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30 CCACACTGCC	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATTG	950
ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	1000
GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCC	TGTGTGTTGA	1050
GGCCTTCACT	GACTACCCAC	CTCTTGGTGC	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
GAAGTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTCGC	100
55 TCATGCTTCA	TTCTACTTCT	CTTCGTAATA	ACACATCACT	CAGACGCTCC	150
CGGTCAACCGT	GATTTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
ATTGCGCCAT	TCTCATCATT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCCT	300
TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60 GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCCTCGG	CCGTATCGAG	ACTGGTGTC	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTTACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTACAC	TGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

2) INFORMATION FOR SEQ ID NO: 437

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAGGAGACC	AAGGCTGGTG	TACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAACTG	300
	TGCCCGTCGG	CCGTGTCGAA	ACCGGTGTCA	TCAAGGCCCG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCCG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTAAAG	GATATCAGAC	GTGGTAACGT	CTGCGGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTTCAACG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCTGGTC	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTA CTGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

50

2) INFORMATION FOR SEQ ID NO: 438

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

```

10 CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
   CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
   CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAACTG      150
   CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
   GTAAAACCTT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
   ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
15 TATTGGCACT GTTCCCGTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCG      350
   GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
   GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT      450
   CGGCTTCAAC GTCAAGAACG TTTCAGTCAA GGAAGTCCGC CGTGGCAACG      500
   TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
20 GCCCAGGTC TCGTCCTTAA CCAGCCCGCG CAGGTTGGCG CTGGTTATGC      600
   CCCAGTCCTC GACTGCCACA CTCGCCACAT TGCTTGCAAG TTCTCTGAGC      650
   TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
   AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
   GCCC                                     754
25

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2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Issatchenkia orientalis*
 (B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

```

45 TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
   CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCTGT CCAATCTCTG      100
   GTTGGGAATG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
   AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
   ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
   CATTAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
50 GTGCCAGTCG GTAGAGTCGA AACCGGTGTC ATTAAGCCAG GTATGGTTGT      350
   CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
   ACCATGAACA ATTAGAACA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
   GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
   CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
55 TTGTCTTGAA CCACCCTGGT CAAATTTCCG CTGGTTACTC TCCAGTCTTG      600
   GATTGTCACA CTGCCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
   GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
   AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC          743
60

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2) INFORMATION FOR SEQ ID NO: 440

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

	CAAGCTCAAG	GCTGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCTCTGT	50
	GGAAGTTTCA	GACCCCTAAG	TACCACGTTA	CCGTCATTGA	CGCTCCTGGT	100
20	CACCGTGACT	TCATCAAGAA	CATGATTACG	GGTACCTCGC	AGGCTGACTG	150
	CGCTATCCTC	ATCATTGCCG	GTGGTACCGG	TGAGTTCGAG	GCTGGTATCT	200
	CGAAGGACGG	TCAGACCCGT	GAGCACGCTC	TGCTCGCTTT	CACCCCTGGGT	250
	GTGCGTCAGC	TCATTGTGGC	CGTCAACAAG	ATGGACACCA	CCAAGTACTC	300
	GGAGGACCGC	TTCAACGAGA	TTGTCCGCGA	AGTGTGGAAC	TTCATCAAGA	350
25	AGGTCGGTTT	CAACCCCAAG	ACTGTTGCCT	TCGTCCCCAT	CTCGGGCTGG	400
	CACGGTGACA	ACATGATCGA	GGCCACCACC	AACATGCCTT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGT	CGGGCAAGGT	CACTGGTAAG	ACTCTGCTGG	500
	ACGCCATCGA	CGCCATCGAG	CCCCCGACCC	GCCCCACTGA	CAAGCCCCCTG	550
	CGTCTCCCTC	TGCAGGATGT	GTACAAGATC	GGTGGTATCG	GTACTGTCCC	600
30	TGTCGGTCGT	GTTGAGACCG	GTGTGATCAA	GCCCGGTATG	GTTGTGACCT	650
	TCGCTCCCTC	GAACGTCACC	ACTGAAGTTA	AGTCGGTTGA	GATGCACCAC	700
	GAGTCGCTCC	CTGAGGGTCT	CCCCGGTGAC	AACGTTGGTT	TCAACGTGAA	750
	GAACGTCTCG	GTTAAGGACA	TTCGCCGTGG	TAACGTTGCC	TCGGACTCGA	800
	AGAACGACCC	CGCTCAGGAG	GCTGCTTCGT	TCAACGCGCA	GGTCATTGTC	850
35	ATGAACCACC	CTGGTCAGAT	CAGCAACGGT	TACTCGCCCC	TGCTTGAAGT	900
	CCACACTGCG	CACATTGCCT	GCCGCTTCAA	CAACATCCTC	CAGAAGATCG	950
	ACCGTCGCTC	GGGTAAGGTG	CTTGAGGAGA	ACCCCAAGTT	CATCAAGTCG	1000
	GGTGACGCTG	CCATGGTGGA	GATGATCCCC	ACCAAGCCCC	TGTGTGTGGA	1050
40	GTCGTTCAAC	GAGTACCCCC	CTCTGGGTCT	TTTCGCTGTG	C	1091

2) INFORMATION FOR SEQ ID NO: 441

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Malassezia pachydermatis*
 55 (B) STRAIN: ATCC 42756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

	ACCACCAAGT	ACTCGGAGGA	CCGCTTCAAC	GAGATTATTC	GCGAGACTTC	50
60	GAACCTTCATC	AAGAAGGTCG	GTTACAACCC	GAAGACTGTT	GCCTTCGTCC	100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCCG	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCCGGTCCG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCCG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTAAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTCCGC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRGTTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
- 30 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTTCGACATG	100
35	TTTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCGG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCCTGTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCCGTGC	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCTTG	GTCGTTTCGC	CGTCCGTGAC	1150

60

2) INFORMATION FOR SEQ ID NO: 443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

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15  GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT      50
    TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA      100
    GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA      150
    CTGTGCTATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA      200
    TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTTGGC YTACACCTTG      250
20  GGTGTTAGAC ARTTGATTGT TGCCGTCAAC AAGATGGACT CTGTCAAGTG      300
    GGACAAGAAC AGATTTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA      350
    AGAAGGTTGG TTACAACCCT AAGACYGTGC CATTCTGTGCC AATYTCTGGT      400
    TGGAACGGTG ACAACATGAT TGAGGCTGCC ACTAACTGCC CATGGTACAA      450
    GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT      500
25  TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC      550
    TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT      600
    GCCAGTCGGC CGTGTCGAGA CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA      650
    CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC      700
    CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCAACGT      750
30  CAAGAACGTC TCCGTTAAGG AGATCAGAAG AGGTAACGTC TGTGGTGA      800
    CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT      850
    GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTTACTCTC CAGTGTGGA      900
    CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA      950
    TTGACAGAAG AACTGGTAAG TCCTTGAGT CYGAGCCTAA GTTCGTCAAG      1000
35  TCGGTTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT      1050
    TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTCCGC GTCAGAGAC      1099
  
```

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

```

55  CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
    GGAAGTTCTGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT      100
    CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG      150
    CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCCAG      200
60  GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCCTGGTG AGTTCGAGGC      250
  
```

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	350
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	400
	AAGTGGTCTG	AGGCCCCGTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACTT	450
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	500
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCCTGG	550
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	600
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCCAGCGACA	650
	AGCCCCCTCCG	CCTTCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	700
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	750
10	CGTGACCTTC	GCTCCTTCCA	ACGTCACCAC	CGAAGTCAAG	TCCGTTGAGA	800
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	850
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	ACGTCGCCGG	900
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	950
	TCATCGTCTT	CAACCACCCC	GGCCAGGTCCG	GTGCTGGCTA	CGCCCCCGTC	1000
15	CTCGACTGCC	ACACCGCCCCA	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1050
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1100
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1150
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1153
20	TGA					

2) INFORMATION FOR SEQ ID NO: 445

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32071

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCG	350
	GTATGGTTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCTTTCAAT	550
50	GCCCAGGTCA	TCGTCTCTAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCACAT	TGCCTGCAAA	TTGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCTTTCCAA	750
55	GCCCATGTGC	GTC				763

2) INFORMATION FOR SEQ ID NO: 446

60 (i) SEQUENCE CHARACTERISTICS:

270

(A) LENGTH: 1346 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 64101

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTGAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTCCCT	TTCGTTCCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCGGTG	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60	AAGTTAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
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	GAAATTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTA CT TCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGGT	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCAC	ACTACCCACC	ATTAGGTCGT	TTGCTGTCA	GAGA	1094

25 2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CAAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCCGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACCTGT	TCCATTCGTT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTTA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA TGCTGCTATT GTTAAATTG TTCCATCAAA ACCATTATCA 1050
 GTTGAAGCTT TCACTGACTA CCCACCATTA GGTCGTTTCG CTGTCAGAGA 1100

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2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG GCCGAGCGTG AGCGTG GTTAT CACCATCGAT ATCGCCCTCT 50
 GGAAGTTCGA GACCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG 100
 TGCTTTTTGT GCTTTTTGTG CCTGTGCCTC GCACAATTCC AGCCCTCGAT 150
 25 AATTATGAAC CTCGTACTAA TATGTCGTTT TCCCACTACC CACAGACGCC 200
 CCCGGCCATC GTGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC 250
 TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG 300
 GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC 350
 CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAAGATGG ACACCAACAA 400
 30 CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAAC TTCA 450
 TCAAGAAGGT CGGCTACAAC CCCAAGGCCG TTCCTTTTCGT CCCCATCTCC 500
 GGTTCACAG GAGACAACAT GCTTACCCCT TCCACCAACT GCCCCGTGTA 550
 CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC 600
 TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG 650
 35 CCCCTCCGTC TTCCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC 700
 TGTGCCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG 750
 TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG 800
 CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA 850
 CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGCAAC GTCTGCGGTG 900
 40 ACTCCAAGAA CGACCCCCCT GCTGCTGCCG CCTCTTTCCA GGCCCAGGTC 950
 ATTGTCTCTA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCCTTCT 1000
 TGACTGCCAC ACTGCCACA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA 1050
 AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC 1100
 AAGTCTGGTG ATGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG 1150
 45 TGTTGAGTCC TTCACCGAGT ACCCCCCTCT CGGTGCTTTC GCCGTCCGTG 1200
 A 1201

50 2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

5
 CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT 50
 GGAAGTTCTGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT 100
 CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG 150
 TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT 200
 10 CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT 250
 GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC 300
 CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA 350
 AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG 400
 CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG 450
 15 ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG 500
 ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC 550
 CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC 600
 CGTCGGTCGT GTCGAACTG GTGTCATCAA GGCTGGTATG GTTGTCACCT 650
 TCGTCTCCTG TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC 700
 20 GAAACCGTCA CTGAAGGTCT CCCCAGTGAC AACGTCGGTT TCAACGTCAA 750
 GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA 800
 AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC 850
 TTGAACCACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG 900
 TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG 950
 25 ACAGACGTTT CCGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT 1000
 GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA 1050
 AGCTTACACT GACTACCCTC CTCTCGGTGC TTTGCTGTT CGTGA 1095

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2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1092 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA 50
 AGTTCGAGAC CCCCAAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT 100
 CGTGATTTCA TCAAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA 150
 50 CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA 200
 GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTTGGT GAGTTCGAGG 250
 CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC 300
 ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT 350
 CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC 400
 55 CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC 450
 GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCTG ACCCCAAGGG 500
 TGTTCCCTTC GTCCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG 550
 AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC 600
 GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC 650
 60 CCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT 700

	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATT	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

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2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCT	CCAGGTTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTCGCTCGGC	900
50	CATTTTTTCA	GTCCTGACCC	CGTTTTGCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	CGGTTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCAA	GGAGCCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCCACATT	GCCTGCAAGT	TCGACACCC	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

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2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
 AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA 100
 GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
 20 CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
 CGTGAGCAGC CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
 CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
 AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
 AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
 25 TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
 AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
 GAGCCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
 TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTGCGC CGTATCGAGA 600
 CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
 30 ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
 TGTTCCCGCG GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
 AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
 GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGCCA 850
 GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
 35 CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
 TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
 CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
 CCCCTCTGGG CCGTTTCGCC 1070

40

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
 ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
 60 GAGATTTTCA CAAGAACATG ATTACTGGTA CCTCCAGGC CGATCTTGCC 150

	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTCGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGGAGGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCCTCTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGATCGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTTCGT	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
20	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092

2) INFORMATION FOR SEQ ID NO: 455

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCAATTG	TATGTTTTCT	CTTTACCTTT	100
	CCCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGTTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAAGTG	650
	TACCACTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	TGCCAACGCT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTTCGA	GCCAACCCCA	AGTTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC C⁻GTCCGTGA⁻ f149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
 CCAGGTCACC GTGATTTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
 25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
 CTTGGTGTCA GACAACCTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300
 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACTTCG 350
 TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTCGT TCCTATCTCT 400
 GGTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
 30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
 CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
 TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
 TCACCTTTGC TCCACCAATG GTCACAACCTG AAGTTAAGTC CGTTGAAATG 700
 35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
 CGTCAAGAAC GTTTCCGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
 ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900
 CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTCGACGAA CTCCTTGAAA 950
 40 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
 AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
 CGTTGAAACC TTCACTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100
 A 1101

45

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

```

5   GTTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
    AGTTCGAGAC CCCCAAGTAC TATGTCACCG TCATCGACGC CCCGGGTCAT      100
    CGTGACTTTA TCAAGAACAT GATCACTGGT ACCTCGCAGG CCGACTGCGC      150
    CATCTTGATC ATTGCCGCCG GTACCGGTGA ATTCGAAGCC GGTATCTCCA      200
    AGGATGGTCA GACCCGTGAG CACGCTCTGC TCGCCTACAC CTTGGGTGTC      250
    AAGCAGCTCA TCGTCGCCAT CAACAAGATG GACACCACCA AGTGGTCCGA      300
    GGAGCGTTTC AACGAAATCA TCAAGGAGAC TTCCAAC TTC      350
10  TCGGCTACAA CCCCAAGGCC GTTCCTTTTCG TCCCCATCTC CGGCTTCAAC      400
    GGTGACAACA TGATTGAGGT CTCCACCAAC TGCCCGTGGT ACAAGGGATG      450
    GGAGAAGGAG TCCAAGGCTG GCAAGGCCAC CGGCAAGACC CTCCTCGAGG      500
    CCATTGACGC CATCGACCCA CCCACCCGTC CCACCGACAA GCCTCTCCGT      550
    CTCCCTCTCC AGGATGTCTA CAAGATCTCT GGTATCGGAA CGGTTCCTGT      600
15  CGGTCGTGTC GAGACCGGTA CCATCAAGGC CGGTATGGTC GTCACCTTCG      650
    CTCCGGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAAAT GCACCACGAG      700
    CAGCTCGCCG AGGGTCTGCC AGGTGACAAC GTTGGCTTCA ACGTCAAGAA      750
    CGTCTCCGTC AAGGAGGTTC GTCGTGGTAA CGTTGCCCGT GACTCCAAGA      800
    ACGACCCGCG CAAGGGTGCC GAGTCCTTCA ACGCCAGGT CATTGTCCTC      850
20  AACCACCTCG TCAGATCGG TGCCGGCTAC GCTCCAGTCT TGGATTGCCA      900
    CACTGCCCAC ATTGCTTGCA AGTTCGCCGA GTTGCTCGAG AAGATCGACC      950
    GTCGTACCGG AAAGTCCATC GAGAACAACC CCAAGTTCAT CAAGTCTGGT     1000
    GATGCTGCCA TCGTCAAGAT GATTCCCAGC AAGCCCATGT GTGTCGAGGC     1050
    TTTACCGAC TATCCTCCTC TGGGTCGTTT CGCTG                       1085
25

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2) INFORMATION FOR SEQ ID NO: 458

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30  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 492 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
35  (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Aspergillus fumigatus
40  (B) STRAIN: DAL-95

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

```

45  TGTCTTCATC CGGAATTGAT TGTGAGTCGT TCCACATGCT CACCTAGTTT      50
    TCGCTCGATC TTTTCACTAA CGCAAACCAT GTAGAACAAC ATTGCCAAGG      100
    CCCACGGTGG TTA CTCCGTC TTA CTGGTG TTGGTGAGCG TACTCGTGAG      150
    GGTAACGATC TGTACCACGA AATGCAGGAG ACTGGTGTC A TTCAGCTCGA      200
    GGGTGAATCC AAGGTCGCAC TGGTGTTCGG ACAGATGAAC GAGCCCCCGG      250
    GTGCCCCTGC CCGTGTGCC CTTACCGGTC TGACCATTCG CGAGTACTTC      300
50  CGTGACCGAG AGGGTCAGGA CGTGCTGCTC TTCATTGACA ACATTTTCCG      350
    TTTACCCAGG GCCGGTCTG AGGTGTCTGC CTTCTCGGT CGTATCCCCT      400
    CTGCCGTCGG TTACCGCCC ACCCTGGCCG TCGACATGGG TGGTATGCAG      450
    GAGCGTATCA CCACCACCAA GAAGGGTTCT ATTACCTCCG TC                       492
55

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2) INFORMATION FOR SEQ ID NO: 459

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60  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1154 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTGGT	ACTCTTGGTA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAACTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GA CTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGCTCTG	800
	TTCCATTTCC	GAATTGGGTA	TCTACCCAGC	TGTCGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAGATC	CAAAGATTCC	TTTCCCAACC	ATTCGCTGTT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55

	CCAATTTCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTACTTTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAAACC	GGTATCAAGG	350
	TTGTGCACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTYGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTCATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCATTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTGCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

25 2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAACCTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCGG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TGCCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTC	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTGCCCCA	900
	TTTGGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTT	AAACAACTTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTC	CTGGTATTCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTC	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

10 2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTT	GCC	AGCT	ATTTT	TG	AAC	GCTTT	TGA	CCT	TGA	AAG	AA	CGG	TGA	AA	AC	50		
	GAC	TTAG	TTT	TAGA	AGTT	G	CCA	ACATTT	TG	GGT	GAAA	ACA	CCG	TCAG	AG	C	100			
	TAT	TGCT	ATG	GAT	GGT	ACT	AAG	GT	TAG	TAG	AGGT	ACT	CC	AGT	TAC	CG	150			
	ATT	CTGG	TGC	TTCA	ATTT	CT	GT	CCC	AGT	CG	GT	AG	AGT	TAC	TT	TAG	GT	200		
30	ATC	TTGA	ACG	TTAT	TGGT	GA	ACCA	ATT	GT	GA	ACA	AGG	T	CAG	TT	GAT	GC	250		
	CA	AGG	AA	AC	AG	CA	AA	AT	T	ACCA	AG	AC	CC	ACC	AG	CAT	T	300		
	CC	AC	CA	AG	G	TGA	AGT	TTT	TG	GAA	ACT	GGT	A	TCA	AGG	TT	G	350		
	G	CCC	CT	TAC	G	CTAG	AGG	TGG	TA	AG	ATT	GGT	TT	AT	TC	GGT	400			
	CGG	TA	AG	ACC	GT	CTTT	AT	CC	AAG	ATT	GAT	TA	ACA	AC	ATT	G	CCA	AG	450	
35	AT	GGT	GGT	TTT	CT	CTG	TTT	T	ACT	GGT	GTC	GT	GAA	AGA	AC	CAG	AGA	AGG	500	
	AAC	GAT	TT	TAT	ATAG	AG	AA	AAT	GA	AGG	AA	ACT	GGT	GTC	ATT	ACT	TG	GA	550	
	TG	ACT	CCA	AG	GT	CG	CCT	TGG	TTTT	CGG	TCA	AAT	GAA	CG	AA	CC	ACC	AGG	600	
	CT	AG	AG	CTAG	AG	TTG	CTTT	A	ACC	GGT	TTAA	CC	ATT	G	CCGA	ATA	CTT	CAG	650	
	GAC	GA	AAG	AAG	GT	CA	AG	ATGT	GTT	ATT	GT	TC	GATA	AA	CA	TTTT	TAG	ATT	700	
40	CAC	CCA	AG	CC	GGT	TCC	G	AAG	TGT	CTG	CTTT	GTT	AGG	TCG	T	ATT	CC	AT	750	
	CT	GT	CGG	TTA	TCA	ACCA	ACC		TTG	CC	ACT	G	AT	ATG	GGT	CT	TTT	ACA	AG	800
	AGA	ATT	ACCA	CC	ACC	ACCA	AA	GGG	TTCC	GTT	ACT	TCT	G	TCC	AAG	CTG	TCT	850		
	CGT	CCC	AG	CC	GAT	GAT	TTAA	CC	GAT	CC	TGC	TCC	AG	CT	ACC	ACT	TT	CG	900	
	ACT	TG	GAT	GC	TAC	CA	CTGT	G	TTG	TCT	CGT	G	TAT	CT	CTGA	ATT	GGG	TAT	950	
45	TAC	CC	AG	CTG	TC	GAT	CCAT	T	GG	ATT	CCAAA	TCC	AG	ATT	GT	TAG	AT	GCT	1000	
	TAT	CGT	TGGT	AA	AGA	AC	ACT	AC	GAA	GGT	TGC	CA	CT	GGT	GTC	CA	ACA	AA	1050	
	TAC	A	AG	CTTA	CAA	AT	CTTTA	CA	AG	AT	ATCA	TTG	CT	AT	TTT	AGG	TAT	GGAT	1100	
	GA	ATT	GT	CTG	AAG	CC	GATAA	ATT	G	ACT	GTC	GAA	AG	AG	CCA	GAA	AG	AT	1150	
	AAG	ATT	CTTG	TCT	CA	ACCA	T	TCG	CC	GTT	GTC	CGA	AG	TTT	TC	ACC	GGT	AT	1200	
50	CAG	G	TAG	ATT	AG	TTAG	ATTG	CA	AG	AC	ACTG	TTAA	AT	CTTT	CA	AGG	AAG	1250		
	TTA	GA	AAG	GTA	AAT	AT	GATCA	CTT	ACC	AG								1278		

55 2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

```

10 TCTGGTCAGA GGCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC      50
   CTGTGCGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CCGTGAACCT      100
   ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC      150
   CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA      200
15 CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG      250
   ATCGGTCTGT TCGGTGGTGC CGGTGTGCGT AAGACCGTGT TCATCCAAGA      300
   ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTCACAG      350
   GTGTGCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG      400
   GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT      450
20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG      500
   GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG      550
   CTGTTTCGTCG ACAACATTTT CAGATTACCC CAAGCCGGTT CAGAAGTCTC      600
   CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG      650
   CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT      700
25 TCCGTCACTT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA      750
   TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT      800
   CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCTGA CCCATTGGAC      850
   TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA      900
   CGTCGCCACA AAGGTCCAAG AAACCTTACA AACTTACAAG TCTCTGCAAG      950
30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA     1000
   ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCTC AACCATTTCG     1050
   TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG     1100
   ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT     1150
   CCAG
35

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2) INFORMATION FOR SEQ ID NO: 464

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

50 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

```

   CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA      50
55 AGAACGGTGA CCAAAACTTG GTTTTGGAAG TTGCCAGCA TTTGGGTGAA      100
   AACACCGTCA GAACATTGCG TATGGATGGT ACTGAAGGTT TGGTTAGAGG      150
   TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG      200
   GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT      250
   GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC      300
60 GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAACC GGTATCAAGG      350

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	TTGTGCACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTT	400
	GGTGGTGCCG	GTGTCCGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTCAACGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATTTTCA	GATTCACCTA	AGCTGGTTCT	GAAGTGTCGG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCT	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTGCA	AGAGCGTATT	ACCACCAACA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTGATC	CTTTGGATTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

2) INFORMATION FOR SEQ ID NO: 465

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 35 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGAGAGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTCG	400
	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTGC	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTTCAG	ATTCACTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCGG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTT	950
	CGAGTTGGGT	ATCTACCCAG	CTGTGACCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAAGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTG	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCACTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
- (B) STRAIN: ATCC 16783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	TATTAAGGTT	300
GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTCGG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCCTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACCTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTTCGGT	CAAATGAATG	550
AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	TTACTTCTGT	800
CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
CTACTTTTCG	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTC	900
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

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5   TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT      50
    CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC      100
    CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA      150
    AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT      200
10  TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC      250
    AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG      300
    TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC      350
    GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCCGGTGG      400
    TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAGTTGATT AACAACATTG      450
15  CCAAGGCCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC      500
    AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA      550
    CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCGGTCAA ATGAACGAAC      600
    CACCTGGAGC TAGAGCCAGA GTTGCCTTGA CCGGTTTGAC TATCGCTGAA      650
    TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT      700
20  TTTCAGATTG ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA      750
    TTCCATCCGC TGTCGGTTAC GAACCTACTT TGGCCACCGA TATGGGTTTG      800
    TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCCGTTA CCTCCGTCCA      850
    AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA      900
    CTTTCGCCCC TTTGGACGCC ACCACCGTGT TGTCCAGAGG TATCTCCGAA      950
25  TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT      1000
    GGACGCTGCC GTTGTCGGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC      1050
    AACAACTTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG      1100
    GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCT AAAGAGCCAG      1150
    AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTCA      1200
30  CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC      1250
    AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG                          1283
  
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35 2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 1287 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*
 (B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

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50  CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA      50
    ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC      100
    ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA      150
    AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCTAGTT GGTAGAGGTA      200
55  CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT      250
    CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT      300
    CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAAACTGGT ATTAAGGTTG      350
    TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCCGT      400
    GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT      450
60  YGCAAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA      500
  
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	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTTCGGT	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTGCAG	650
	AATATTTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTCCGC	CACCTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

20 2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTC AAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
40	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACCTGAAGCT	GAAGTTTGGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTCA	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCGTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCGTCA	CCAGCAACCA	900
	CTTTCGCCCA	C'TTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTGCTG	GTTGTGCGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCTTTT	CCCAACCTTT	CTCCGTGCGA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTT	1250

5 2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20 AGGTGCTCT GTCAGTACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTG GAACAATCCA CTTCTGCTGA AGTTTGGAG ACTGGTATCA 200
25 AGGTTGTCGA CTTGTTGGCC CTTACGCCA GAGGTGGTAA GATTGGTTTG 250
TTCGGTGGTG CCGGTGTCGG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCACG GTGGTTTCTC TGTTTTCACT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
30 GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTTCGTT 550
GACAACATT TCCAGATTCAC CCAGGCCGCT TCTGAAGTGT CTGCTTTGTT 600
GGTTCGTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
35 TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTTGGTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAACTTTGC AAGCTTACAA GTCTTTGCAA GATATCATTG 950
40 CCATTTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTGTCT CAACCATTCG CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTGT GACGGTAAGT ACGACCACTT 1140

45

2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
60 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAAG	TTGCTCAACA	TTTAGGTGAA	100
5	AACACCGTCA	GAACCATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTACTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTC	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTCGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	ACACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTACTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAACCC	GGTATTAAAGG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTGACTGGT	TTGACCATTG	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTGTTGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGAA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

15

2) INFORMATION FOR SEQ ID NO: 473

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1285 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida rugosa*
- (B) STRAIN: ATCC 96275

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTGC	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACTGGTGTC	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCACCG	GTGACCCTGT	AGACGAGCGT	250
	GGTCCCGTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGTC	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTACTCGTGA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCCGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCGCC	TTGGTGTTCG	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTTCGTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCTT	TCCGCTGTCG	GTTACCAGCC	TACCCTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCCCTGC	900
	CACCACCTTC	GCCCATTGGG	ATGCCACCAC	TGTCTTGTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTCGACC	CTCTCGACTC	CAAGTCCCCT	1000
	CTTCTTGACG	CCGCTGTCGT	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAGGAT	ATCATTGCCA	1100
55	TTCTTGGTAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCCAG	CCTTTCGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAAGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

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2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG TCAATTGCCA GCTATTTTGA ACGCTTTGGA AATCGACACT 50
 CCAGAAGGAA AGTTGGTTTT GGAAGTCGCT CAACATTTGG GTGAAAACAC 100
 20 TGTCAGAACC ATTGCTATGG ATGGTACTGA AGGTTTAGTC CGTGGTGAAA 150
 ACGTTTCTGA CACTGGTGCT CCAATTTCCG TCCCAGTTGG TAGAGAAACC 200
 TTGGGTAGAA TTATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGTCC 250
 AATCAACTCC AAGATGAGAA AGCCAATTCA TGCTGATCCT CCATTATTCG 300
 TTGAACAATC CACTGCTGCT GAAGTTTTGG AAAGTGGTAT CAAGGTTGTC 350
 25 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTTCGGTGG 400
 TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAATTGATT AACAACATTG 450
 CCAAGGCTCA TGGTGGTTTC TCTGTCTTCA CTGGTGTCGG TGAAAGAACC 500
 AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACTG GTGTTATCAA 550
 CTTGGAAGGT GATTCTAAGG TCGCGTTGGT TTTCGGTCAA ATGAACGAAC 600
 30 CTCCTGGAGC TAGAGCTAGA GTCGCCTTGA CTGGTTTGAC CATCGCTGAA 650
 TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGTTGTTTA TCGACAACAT 700
 TTTTCAGATC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
 TTCCATCCGC TGTCGGTTAT CAACCAACTT TGGCCACCGA TATGGGTTTG 800
 TTGCAAGAAA GAATTACTAC CACCAAGAAG GGTTCCGTCA CTTCTGTCCA 850
 35 AGCCGTTTAC GTGCCAGCTG ATGATTTGAC TGATCCTGCT CCAGCTACCA 900
 CTTTTCGCGCA TTTGGATGCC ACCACTGTGT TGTCCAGAGG TATCTCTGAA 950
 TTGGGTATCT ACCCAGCTGT CGATCCTTTG GATTCCAAAT CTAGATTGTT 1000
 GGATGCTGCC GTCGTTGGTC AAGAACATTA CGATGTCGCT ACTCAAGTTC 1050
 AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100
 40 GGTATGGATG AATTGTCCGA ACAAGATAAG TTGACCGTCG AAAGAGCTAG 1150
 AAAGATTCAA AGATTCTTGT CTCAACCTTT CGCTGTGCTG GAAGTCTTCA 1200
 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CTCTTCTTTC 1250
 AAGGCTGTCT TGGACGGTAA GTACGATCAC TTG 1283

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2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTTCG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCTG	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTCCGGTGGT	400
	GCTGGTGTCTG	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTAC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCGA	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATT	GCTGTTGCCG	AAGTTTTTCA	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

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2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCTGATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGTC	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCTG	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCCACG	GTGGTTTTCTC	450
	TGTTTTCAAC	GGTGTCCGGT	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCCTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCGGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCACT	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCTG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTGCGAG	AGAGCCAGAA	AGATTCAGCG	TTTCCTTTCC	1150
	CAGCCATTCTG	CTGTGCGTGA	GGTTTTACCC	GGTATCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTGT	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

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2) INFORMATION FOR SEQ ID NO: 477

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1296 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida viswanathii*
- (B) STRAIN: ATCC 28269
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTGCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGCG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTCACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAAGCC	GGTATCAAGG	350
40	TTGTGCACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTGACTGGT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGTCTG	CTTTGTGTTG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTTCG	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGCTT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGCGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGCTT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

TCAATTCGAG CAAGGCAACC TCCCTGCCAT CTTGAACGCT CTCACCTTGA 50
 AGAATGGTGA CAACGACTTG GTTTTGGAAAG TTGCCCAGCA CTTGGGTGAG 100
 20 AACACCGTCA GAGCCATTGC CATGGATGGT ACCGAGGGTT TGGTTAGAGG 150
 TGCCTCCGTC AAGGACACTG GCGCCCCTAT CTCGGTCCCC GTTGGCCGCG 200
 GGACTTTGGG TCGTATCATC AACGTCACCG GTGACCCCAT TGACGAGAGA 250
 GGTCCCATCG AGCTGACCCA GAGAAACCC TATCCACGCCG ACCCCCCCTC 300
 GTTCGTTGAG CAGTCCACCA ACGCTGAGGT TTTGGAGACT GGTATCAAGG 350
 25 TTGTCGATTT GTTGGCTCCC TACGCCAGAG GTGGTAAGAT TGGTTTGTTC 400
 GGTGGTGCCG GTGTCGGTAA GACCGTCTTC ATTCAGGAGT TGATCAACAA 450
 CATCGCCAAG GCCCACGGTG GGTTCCTCGGT CTTCACTGGT GTCGGTGAGA 500
 GAACTAGAGA GGGTAACGAC TTGTACCGTG AGATGAAGGA GACCGGTGTC 550
 ATCAACTTGG AGGGTGACTC CAAGGTGGCC TTGGTGTTTCG GTCAGATGAA 600
 30 CGAGCCCCCT GGAGCCAGAG CCAGAGTCGC CTTGACCGGG TTGACCATTG 650
 CCGAATACTT TAGAGACGAG GAGGGTCAGG ATGTGTTGTT GTTCGTTCGAC 700
 AACATCTTCA GATTACCCA AGCTGGTTCG GAGGTGTCGG CTTGTTGGG 750
 TCGTATTCCC TCTGCCGTCG GTTACCAGCC CACCTTGGA ACTGATATGG 800
 GATTGTTGCA GGAGCGTATC ACCACGACCA AGAAGGGTTC CGTCACCTCA 850
 35 GTGCAGGCCG TCTACGTCCC CGCTGATGAC TTGACTGACC CTGCTCCCGC 900
 CACCACCTTT GCCCACTTGG ACGCCACCAC CGTGTTGTCC AGAGGTATCT 950
 CTGAGTTGGG TATCTACCCC GCCGTCGACC CTTGGACTC CAAATCGAGA 1000
 TTGTTGGACG CTGCCGTGGT CGGTCAGGAG CACTACGATG TTGCCTCGAA 1050
 CGTCCAGCAG ACCTTGCAGG CCTACAAGTC CTTGCAGGAT ATCATTGCCA 1100
 40 TTTTGGGTAT GGATGAGTTG TCCGAGGCTG ACAAGTTGAC CGTTGAGAGA 1150
 GCCAGAAAGA TCCAGAGATT CTTGTCGCAG CCCTTCGCTG TTGCCGAGGT 1200
 TTTCATGGT ATCAAGGGTA GATTGGTCAG ATTGGAGGAC ACCGTCAGAT 1250
 CTTTCAAGGA GGTTTTGGAG GGTAAGTACG ACCACTTGCC CGAGA 1295

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2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

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TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG      100
5  TTTACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA      150
AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCCGTG CCGTGTGTC      250
CTTACCGGTT TGACCATTGC TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
10 TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTCACTCAA      400
GCTGGTCTTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCCG      450
TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA      500
CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                        534

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2) INFORMATION FOR SEQ ID NO: 480

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(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 494 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Cryptococcus albidus
    (B) STRAIN: ATCC 66030

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

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CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
35 TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
GAGGGTGA CT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC      250
TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT      300
TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTTATTGA CAACATTTTC      350
40 CGATTCACCC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC      400
CTCCGCCGTC GGTACCAGC CCACTCTGTC CACCGACATG GTTACCATGC      450
AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC            494

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2) INFORMATION FOR SEQ ID NO: 481

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(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 415 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

55

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(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Fusarium oxysporum
    (B) STRAIN: WSA-212

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

295

	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTCGG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCGG	TTACCAGCCC	350
	ACCCTCGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

2) INFORMATION FOR SEQ ID NO: 482

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAAGC	TCGTTCTCGA	GGTTGCCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTACTGAGGG	TCTCGTCCGT	GGTCAGCCCCG	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATTG	CCGTGCGTCG	TGGTACTCTT	200
	GGTAGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	CTCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTGCGAT	350
	CTCCTTGCCC	CCTACGCCCC	TGGTGGTAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTTT	TCATTCAGGA	GCTGATTAAC	AACATTGCCA	450
	AGGCCCCATG	TGGTTTCTCC	GTTTTACCCG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCG	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCC	TGCCCGTGTT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGGTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATTC	750
45	CCTCCGCTGT	CGGTTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCTT	GCTACCACCT	900
	TCGCCCATT	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGA	1000
50	TATCACCGTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCCCGTA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	ACACTGTTCG	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

2) INFORMATION FOR SEQ ID NO: 483

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

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15  ATTCAAGAAT TGATCGTACG TTCCTCCGCC CCACACACGA TCAATGGAGA      50
    AAGAAACAAA TTTTGTGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA      100
    ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTCAC TGGTGTCCGC      150
    GAGCGGACCC GTGAAGGAAA TGACTTGTA CACGAAATGC AGGAAACCCG      200
    TGTATCCAG CTCCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA      250
20  TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC      300
    GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA      350
    TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC      400
    TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG      450
    TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCCACCCT      500
25  CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACCCT ACCACCAAGG      550
    GCTCCATCAC CTCTGTGCAR GCCGTCTACG TCCCCG      586
  
```

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

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45  GCGTGGCCAG AAGGTCATTG AACTGGGTGC TCCCATCACC ATCCCCGTGC      50
    GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC      100
    GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC      150
    CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA      200
50  TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT      250
    CTGTTCCGGT GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT      300
    CAACAACATC GCCAAGGCC ACGGTGGTTT CTCCGTGTTC ACTGGTGTGC      350
    GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT GATTGAAACC      400
    GGTGTCATTA ACCTCGAGGG TGACTCGAAG GTGGCTCTGG TGTTCCGTCA      450
55  GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA      500
    CTGTGGCCGA GTACTTCCGT GACGACGAGG GCCAGGATGT GCTGCTGTTC      550
    ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCCGAGA CTTCCGGCTCT      600
    GCTGGGTCGT ATCCCTTCGT CGGTGCGTTA CCAGCCCACT TTGTCGACCG      650
    ATATGGGTGC CATGCAGGAG CGTATCACCA CCACCAAGAA GGGTTCGATT      700
60  ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC      750
  
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	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTCCG	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

10

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1261 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Malassezia pachydermatis*
(B) STRAIN: ATCC 42756

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTTCGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCCTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCCG	TAACGGTACC	TTGGGCGGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTCG	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGGTG	TGCYGGTGTY	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTC	CTGGTGTCCG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCCG	GTCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCCGAGAC	TTCGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCCA	900
	CTTGGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCGYAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCCGA	GGAGGACAAG	CTCACTGTCC	AGCGTGCCCC	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTCT	1250
	TGTCCGGTAA	G				1261

55

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 1282 bases

298

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*

(B) STRAIN: DSM 70336

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAAGT	TGGTCTTGGA	GGTGGCCCAG	CACTTGGGTG	AGAACACCGT	100
15	CAGAACCATT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
	TCACCGACAC	YGGTGCCCT	ATCTCCGTGC	CTGTGCGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTCACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGAGAG	CTGGTATCAA	GGTTGTGCGAC	350
20	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
	CGGTGTGCGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAAAC	AACATTGCCA	450
	AGGCCACGG	TGGTTTCTCC	GTTTTACCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTCG	CCTTGTTTTT	CGGTCAGATG	AACGAGCCTC	600
25	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
30	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
	TCGCCCCTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTGCA	CCCCTTGGAC	TCCAACCTCCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGCAGG	ATATCATTGC	CATTTTGGGT	1100
35	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTTCAC	1200
	CGGTATTGAG	GGTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

40

2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 482 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*

(B) STRAIN: WSA-214

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAACAAC	ATTGCCAAGG	CTCACGGTGG	100
60	TTACTCTGTC	TTCATGGTGT	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150

	TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200
	AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCG	GTGCCCGTGC	250
	CCGTGTCGCT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
	AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
5	GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCC	CTGCCGTCGG	400
	TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
	CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1290 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Pichia anomala</i>
(B)	STRAIN: ATCC 18205

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

	TCGAACAAGG	TAACTTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
	CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
	CACGTGCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTTCGTGGTG	150
30	AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
	ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
	TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
	TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
	GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAATATG	GTTTATTCGG	400
35	TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
	TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
	ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
	TAACTTGGA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
	AACCACCAGG	TGCTAGAGCT	CGTGTTGCTT	TAACTGGTTT	GACCATGCT	650
40	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
	CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
	GTATTCCATC	TGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
	TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTCAG	TTACTTCTGT	850
	CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
45	CCACTTTCGC	CCATTTGGAT	GCTACTACTG	TCTTGCTCTG	TGGTATTTCA	950
	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
	ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
	TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
	TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
50	AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
	TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
	TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

55

2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1291 bases
60	(B)	TYPE: Nucleic acid

300

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTTCGAA	CAAGGTAAC	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTTTAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG	150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC	200
	GTGAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA	250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC	300
	TTCATTCACT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA	350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA	400
20	TTCGGTGGTG	CCGGTGTCCG	TAAAACGTGC	TTTATCCAAG	AATTGATTAA	450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTCACC	GGTGTGGGTG	500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAAACTGGT	550
	GTTATTAAC	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT	600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA	650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT	700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAGTTT	CTGCCCTTAT	750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA	800
	TGGGTTTGT	ACAAGAACGT	ATTACCACCA	CACAAAAGG	TTCAGTTACT	850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC	900
30	AGCTACCCT	TTGCCCCATT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA	950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGTCTG	ATCCATTAGA	TTCTAAATCA	1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC	1050
	CAACGTTCAA	CAAACCTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG	1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GAATGTCGAA	1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTG	CTGTTGCCGA	1200
	AGTTTTCACT	GGTATCCCAG	GATGATTGGT	TAGATTAAAA	GACACTATCA	1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A	1291

40

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 508 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
(B) STRAIN: ATCC 10658

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCCTTA	CAGCAAGCTT	ATAAAGGAGC	50
	GAAAAAGATC	TGACATTCGG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA	150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG	200

TCATTCAGCT CAAGAACGAC AAGTCCAAGG CCGCTCTGGT CTTCCGGACAG 250
 ATGAACGAGC CCCCCGGAGC TCGTGCCCGT GTCGCTCTGA CCGGTCTCAC 300
 CATCGCCGAG TACTTCCGTG ACGTCGAAGG ACAGGATGTG CTACTCTTCA 350
 TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCAGAGGT ATCTGCCCTG 400
 5 CTCGGACGTA TCCCATCTGC TGTCGGATAC CAGCCCACAC TCTCAACCGA 450
 TATGGGTGGT ATGCAAGAGC GAATCACAAC CACCAAGAAG GGTTCGATTA 500
 CCTCCGTC 508

10

2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 686 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula mucilaginosa*
 (B) STRAIN: ATCC 66034

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

TGTCCTCATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCGGTCTT CACCGGTGTC GGCAGCGTA CCCGTGAGGG TAACGGTGAG 100
 TCTCCCCCTT CAAACTTTTG GCCGGCTAGT TGGCGCAGCG CAAACTGACG 150
 30 CGCGCGCCCT GTCCAGACTT GTACCAGAG ATGATCGAGA CTGGTGTCAT 200
 CCAGCTCGAG AACGACAACT CGAAGTGCGC TCTCGTGTTT GGCCAGATGA 250
 ACGAGCCCCC TGGTGCCCGT GCCCGTGTCG CTCTCACTGG GTTCGTCCTT 300
 TCTCTCTCTC GAGCGTCCTG GCTTGATACG GAACGCTGAC ACGTCACGCA 350
 GTCTCACTAT TGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGACGTGCTC 400
 35 CTCTTCATCG ACAACATCTT CCGTTTCACC CAGGGTGAGC CGCCTCCGCG 450
 GGCATTCTCC CGTTTCTTTC GCGCTGACGT CTGTCCCGTA TAGCCGGTTC 500
 GGAGGTGTCT GCCCTTCTCG GACGTATCCC GTCCGCTGTC GGATACCAGC 550
 CGACTCTCTC GACCGACATG GGTCAGATGC AGGAGCGTAT CACGTAAGTT 600
 TGGCCGCAGC TCCGTCCGCG GCGCCCTTTG TGTCTGACCG TGTTCACCG 650
 40 CTCAGCACCA CCAAGAAGGG CTCGATCACC TGTGTC 686

45

2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60 TGTCTTGATT CAGGAGCTCA TCAACAACGT CGCCAAGGCC CACGGTGGTT 50

	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCGTGCCCC	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTACTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCC	TCCGCTGTCTG	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTTCGCCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

15

2) INFORMATION FOR SEQ ID NO: 493

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1211 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTGCGCCC	CGGTACCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCAT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCACGG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTACAGT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGTT	450
	CGGTCAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCGTGTC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCGCTGAC	800
	GATCTGACGG	ATCCC GCCCC	CGCCACCACC	TTGCCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCAGAGTA	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTCTG	900
	ACCCCCTCGA	TCCCAAGTCG	CGTATGTGG	ACCCCCGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTGCGGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

60

2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC 50
 CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA 100
 ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC 150
 20 TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA 200
 CCGGTATTAA GGTGTGCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG 250
 ATTGGTCTTT TCGGTGGTGC CGGTGTGCGT AAGACTGTGT TCATTCAGGA 300
 GCTTATTAAAC AACATTGCTA AGGCCCACGG TGGTTACTCT GTCTTCACTG 350
 GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG 400
 25 GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT 450
 CGGTCAGATG AACGAGCCTC CAGGAGCCCCG TGCCCGTGTT GCCTTGACCG 500
 GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG 550
 TTGTTCAATTG ACAACATTTT CCGATTACC CAGGCCGGTT CTGAGGTCTC 600
 TGCCTTGTTG GGTCTGTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG 650
 30 CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT 700
 TCCGTACACT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA 750
 TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT 800
 CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCCTCTTGGT 850
 TCCAAGTCCC GTCTTTTGGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA 900
 35 CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG 950
 ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC 1000
 ACTGTGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC 1050
 CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG 1100
 ACACCATCCG ATCCTTCAAG GAGATCCTTG AC 1133

40

2) INFORMATION FOR SEQ ID NO: 495

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 55 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
 60 GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTGC 100

	AGTATTAATT	GTGTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCCG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCGT	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAATTTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCATCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGCTC	GTATCCCATC	TGCCGTCGGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTGTTATTCAA	GAACATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTCG	AAAGGCTCAT	GGTGGTTACT	100
	CCGTGTTCAC	TGGTGTCCGC	GAGCGAATC	GTGAGGGTAA	CGACTTGATC	150
	CACGAAATGC	AGGAGACCTC	TGTCATTGAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAAA	TGAACGAACC	TCCTGGTGGT	CGTGCTCGTG	250
	TTGCTCTGAC	TGGGTAAGTT	GTTCTTCGCG	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGCTC	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTTCTTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGGT	550
	GTGAGAAGTG	CGCCGGAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTCTGATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGBAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

```

5      TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
      CCGTCGGCCG AGGTACCCTT GGTCTGAATCA TCAACGTCTG TGGTGAGCCC      100
      ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC      150
      TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA      200
10     CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG      250
      ATTGGTCTCT TCGGTGGTGC CGGTGTGGGT AAGACTGTCT TCATCCAGGA      300
      GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG      350
      GTGTCCGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG      400
      GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT      450
15     CGGTCAGATG AACGAGCCTC CCGGAGCCCC TGCCCCGAGTC GCCCTTACTG      500
      GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG      550
      CTCTTCGTTG ACAACATTTT CCGATTACAC CAGGCCGGTT CCGAGGTGTC      600
      CGCTCTGCTT GGTCTGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG      650
      CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT      700
20     TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA      750
      TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCCTGT      800
      CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT      850
      TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAGG AGCACTACGA      900
      TGTTGCTTCC AACGTCCAGC AGACCCTCCA GGCTTACAAG TCTCTCCAGG      950
25     ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG      1000
      ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC      1050
      CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG      1100
      ACACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC      1148
  
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30

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

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35     (A) LENGTH: 966 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Aspergillus fumigatus
      (B) STRAIN: WSA-172
  
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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

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      GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
      CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC      100
50     CCAGACTCGT GAGCATTTCG TGCTCGCCCG CCAGGTTGGT GTCCAGAAGA      150
      TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG      200
      GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA      250
      GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG      300
      GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT      350
55     GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTCTT      400
      GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT      450
      CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTTGAGATT      500
      GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC      550
      CTTCAAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC      600
60     TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCATTGCT      650
  
```

	GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700
	CCTGACCGAG	GCGGAGGGTG	GTCGTCGTAC	TGGCTTCGGT	GCCAACTACC	750
	GTCCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTTCCCGCA	CACCGTGTCC	800
	AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
5	TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
	GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
	GCTGGTCAAC	GCTTCA				966

10

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 846 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Blastoschizomyces capitatus</i>
(B)	STRAIN: ATCC 10663

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
	GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTTAAGCA	CATTGTTGTT	100
	TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAACCTGT	150
30	CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
	ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
	CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
	ATACATTCCT	ACCCAGTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
	TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTACTGTTGC	CACTGGACGT	400
35	GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
	CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
	AGGAACTTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
	GGTGTTAAGC	GTGAAGACCT	TAAGCGTGGT	ATGGTTGTTG	CTAAACCAGG	600
	TACCGTTAAG	CCACACACCA	AGTTCCTTGC	CTCCATCTAT	GTTTGGACTA	650
40	AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACTA	CAGACCTCAA	700
	CTTTTCCTTG	TGTTCTGCTGA	TGTTACCACCT	GTCTTGACCT	TCCCAGAGGG	750
	TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
	GCGAACTTGT	TCACCCAGTT	GCTGTGGAAC	AAGGCCAACG	TTTCAA	846

45

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

50	(A)	LENGTH: 846 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Candida rugosa</i>
(B)	STRAIN: ATCC 96275

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

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GGTGCCATTA TTGTTGTTGC TGCCTCTGAT GGACAGATGC CCCAGACCCG      50
TGAGCATCTT TTGCTTGCCC GCCAAGTCGG TATGCAAAAG GTCGTTGTGT      100
5  TTGTTAACAA GATTGATACC ATTGATGACC CTGAAATGCT TGATCTTGTC      150
GAGATGGAGA TGCCTGAAC TTTGAATGAA TATGACTTCG ATGGAGATAA      200
CTCTCCTGTC ATTATGGGCT CTGCTCTTGC TGCTCTTGAG GACAAGAACC      250
CCGAGATTGG TAAGGACCGT ATCATGCAGC TCTTGGACGC TGTGATGAA      300
TGGATCCCTA CCCCCGAGCG TGACCTTGAC AAGCCTTTCA TGATGCCTAT      350
10 TGAGGCCTCT TTCTCCATTT CTGGTCGTGG TACTGTTGCC ACTGGCCGTG      400
TCGAGCGTGG TATTCTCAAG AAGGGTGAGG AAGTCGAGAT CGTTGGTTTC      450
AACAAGCAGC CCCTGAAATC TGTGTGTTACT GGTATTGAAA TGTTCAGAA      500
GGAACCTTGAT CAGGCCCAGG GCGGTGATAA TGCTGGTATC TTGCTTCGTG      550
GTATTCGTCG TGAGGACTTG CAGCGTGGTA TGGTTTTTGGC CAAGCCTGGA      600
15 ACTGTTAAGG CTCACACCAA GTTCCTTTCC TCCATCTACG TTCTCTCCAA      650
GGAAGAGGGC GGCCGTCAC TCTCTTTTCGG TATGAACTAT CGTCCCCAGA      700
TGTTTCGTTTC TGCAGCTGAT GTCACCGTTA CTCTTACTTT CCCTGAGGGT      750
GTTGAACAGC AACTCAGGT CTTCCCTGGT GAGAACACCG AGATGGTTGG      800
CGAGCTCGTT CACCCTACTG CTATTGAGGT TGGTCAACGC TTCAAC      846
20

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2) INFORMATION FOR SEQ ID NO: 501

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 944 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Coccidioides immitis
35 (B) STRAIN: Silveira

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

```

AGTTGTCGTC GTTGCTGCTT CAGACGGTCA AATGTATGCA ACCGAGAGCA      50
40 CTCCCGGATC TTGGTTTAAA TGGCACTAAT ATAAGACAGG CCTCAAACCTC      100
GAGAGCATTT ACTTCTCGCC CGTCAGATCG GTATCCAAAA AATCGTCGTC      150
TTCGTGAACA AGGTTGATGC CATCGAGGAC AAAGAGATGT TGGAGCTTGT      200
TGAATTGGAG ATGCGTGAAC TCCTAACCAG CTACGGTTTC GAGGGTGAAG      250
AAACTCCCAT CATTTTTTGGC TCTGCTCTCT GTGCCCTCGA AGGAAGACAA      300
45 CCCGAGATCG GTGTTACCAA GATTGATGAG CTCTTGCAGG CCGTCGACAC      350
CTGGATTCCC ACTCCTCAGC GTGAGACTGA CAAGCCCTTC TTGATGTCCA      400
TTGAGGAAGT GTTCTCTATT TCCGGACGAG GAACCGTTGT CTCCGGCCGT      450
GTGGAGCGTG GTATCCTCAA GAAGGACTCC GAAGTTGAAA TTGTCGGCGG      500
TTCGCCCGAG CCAATCAAAA CCAAGGTTAC CGATATCGAA ACCTTTAAGA      550
50 AGTCTTGCGA CGAGTCTCGC GCTGGTGATA ACTCCGGCTT GCTCCTACGA      600
GGCGTTAAGC GTGAAGATAT TAGCCGTGGC ATGGTCGTCG CTGTACCAGG      650
AAGTGTC AAG GCCCATACTG AATTCTTAGT TTCGCTTTAC GTCCTCACC      700
AAGCTGAGGG TGGGCGCAAA TCTGGATTCA GCAGCAAGTA CCGCCCACAG      750
ATGTTTCATT GCACCTGCGG TATGTAATAC TGTGATAATT TCGTTGACAT      800
55 GGTACTGATT GAATTCTATA GACGAAGCGG CTCAGCTCAG CTGGCCCCGA      850
GAAGATCAAG ACAAGATGGC TATGCCAGGA GACAATATCG AAATGATTTG      900
CACCACCTTG CACCAGTTG CCGCCGAGGC TGGCCAGCGA TTCA      944
60

```

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 849 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA 50
ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG 100
TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG 150
20 ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC 200
TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG 250
AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG 300
ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA 350
GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG 400
25 AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG 450
CAGGAGGTTA TCAAGACCAA GGTTACCGAC ATTGAGACCT TCAAGAAGTC 500
TTGTGAGCAG TCCCAGGCTG GTGACAACCTC TGGTCTCCTC ATCCGAGGTG 550
TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC 600
GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA 650
30 GGAGGGTGGC CGACACACCG GTTTCAGGA GCACTACCGA CCCCAGCTCT 700
ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT 750
GAGGATGCCT CCAGTAAGAT GGTCATGCCT GGTGACAACA CCGAGATGGT 800
TGTCACCATG GGTCACCCCA ATGCCATCGA GGTTGGTCAG CGATTCAAC 849

35

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1064 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: G186A5

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG 50
CGAGGGACTG CTGAGGGTTT TATGCTTTTT AGGCCCCCTT GTTTCTGAGA 100
55 GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT 150
GAGCATTTGC TCCTTGCCCC ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT 200
CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG 250
AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG 300
ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC 350
60 TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT 400

	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT	450
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTGAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAAGTG	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCTGGGCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTCGGC	CAGAACTATC	GTCTCTAAAT	800
	GTTTCATCCG	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAACTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
	CGGCCAGCGA	TTCA				1064

2) INFORMATION FOR SEQ ID NO: 504

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Paracoccidioides brasiliensis*
 - (B) STRAIN: ATCC 32071
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	GCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAAGTC	150
	GGTGTTTACA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TCGAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGGATA	CTTGGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTCGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTCAT	800
50	TCTTTCACTA	TATTCCTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTG	ATGCCCCGGT	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982

2) INFORMATION FOR SEQ ID NO: 505

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 931 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCGTC	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGATATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACCTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCTGC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACCTC	TTGGTCTCCA	TGTATGTCTT	GA CTGAGGCT	700
	GAAGGTGGTC	GTCGTACTGG	ATTCGGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTACT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCAGT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAACCTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAAAC	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500

	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550
	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCCTCA	700
5	TTATTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTAAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 964 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trichophyton mentagrophytes</i>
	(B)	STRAIN: WSA-225

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAG	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
30	GGTCGTTTTC	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAACCTC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
35	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCCGAC	GTCGAAATTG	500
	TTGGTGGCTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAACT	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
40	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGATG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGTTAT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTCAG	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
45	GACAACGTCG	AGATGATTG	CAAAACCCTC	CACCCCATTG	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

50 2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 844 bases
	(B)	TYPE: Nucleic acid
55	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

5 GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTCGAAGC CCCAGACCCG 50
 AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT 100
 TTGTTAACAA GGTTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT 150
 GACATGGAGA TGCAGATCT GCTGACCCAG TACGGTTTGT ATGGTGACAA 200
 10 CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA 250
 AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG 300
 CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCGT 350
 TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG 400
 TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTTGGCTAC 450
 15 AACAACAAGC CCATCAAGGC TGTTGTTACC GGTATTGAGA TGTTCAAGAA 500
 GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG 550
 GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC 600
 ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC 650
 CGAGGAGGGT GGTGGAACCA GCTCTTTTCG CGCCAACCTAC CGACCCGAGA 700
 20 TGTTCAATCCG AACTTCTTCC GTCACCGCCA CTCTCACCTT CCCCAGGGT 750
 ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT 800
 CGAGCTTGTT CACCCTACCG CCATTGAGGT CAACCAGCGA TTCA 844

25

2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1067 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

CTTGGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA 50
 CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC 100
 CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC 150
 45 CGATGTTGCT ATGCTTGTCG TGCCCCCGCA GGCTGGTGGT TTCGAAGCTG 200
 CTTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC 250
 CTTGGTGTCA AGCAGATCAT TTGCGCCATC AACAAGATGG ACAAGTGCGA 300
 CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC 350
 TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC 400
 50 GGTTCATGG GTGACAACAT GGTTGAGCGC TCCACCAACA TGCCGTGGTA 450
 CAAGGGCAAG ACCTTGGTG AGGCCCTCGA CATGATGGAG CCCCCGAAGA 500
 GGCCCGTCGA CAAGCCCCTG CGTCTTCCCC TCCAGGGTGT GTACAAGATC 550
 GGTGGTATCG GTACCGTCCC TGTCGGTCGT GTGGAGACTG GTCAGCTCAA 600
 GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA 650
 55 AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC 700
 AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG 750
 TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCCT 800
 TCACCGCCCA GGTCATCATC TTGAACCACC CTGGTACCAT CAAGGCCGGT 850
 TACTCCCCTG TGGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA 900
 60 CGAGATCACC AGCCGTATGG ACAAGCGTAC CGGTAAGGCC CTTGAGGAGA 950

ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000
TGCAAGCCCA	TGGTCGTCGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCTG	1050
TTTCGCCGTG	CGTGACG				1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA	ACGTGGTATT	ACTATTGATA	TTACCTTATG	GAAGTTCGAG	50
ACCACCAAGT	ACTACTACAC	CGTCATTGAT	GCCCCCTGGTC	ACCGTGACTT	100
25 CATCAAGAAC	ATGATTACGG	GTACTTCTCA	AGCCGATGTT	GCTATGCTTG	150
TTGTACCAGC	TGAGGCTGGT	GGTTTCGAGG	CCGCTTTCTC	CAAGGAAGGA	200
CAGACCCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTTGGTG	TCAAACAGAT	250
CATCTGTGCC	ATTAACAAGA	TGGACAAGTG	CGACTACAAG	GAGGACCGTT	300
ACAGTGAAAT	CCAGAAGGAA	GTCCAGGGTT	ACCTCAAGAA	GGTCGGTTAC	350
30 AATATTGAGA	AGGTGCCCTT	CGTTGCCATC	TCCGGTTTCA	TGGGAGACAA	400
CATGGTTGAG	CGTTCCACCA	ACATGCCCTG	GTATAAGGGA	AAGACATTGG	450
TCGAGGCCCT	TGATCAGATG	GAACCCCCAA	AGAGGCCCGT	TGACAAGCCA	500
CTTCGTCTTC	CCCTCCAGGG	TGTCTACAAG	ATCGGTGGTA	TCGGTACCGT	550
CCCCGTCGGT	CGTGTGAAA	CTGGTATGTT	GAAGGCTGGT	ATGATTCTAA	600
35 CCTTTGCTCC	TAACCCAATC	ACCACTGAAT	GCAAATCCGT	TGAAATGCAC	650
CACGAAACCG	TTGAGGTTGC	TTACCCCGGT	GACAACGTCG	GTTTCAACGT	700
AAAGAACGTT	TCTACTTCTG	ACATTCGCAG	TGGTCACGTT	GCCTCTGATT	750
CTAAGAACGA	CCCTGCCAAG	GCTGCTGTTT	CCTTCACTGC	CCAGGTCATT	800
GTGCTCAACC	ACCCTGGTAC	CATTAAGGCC	GGTTACTGCC	CCGTCGTCGA	850
40 TTGCCACACC	GCTCACATT	CATGTAAATT	CGAAGAGATC	ACCAGCCGTA	900
TGGACAAGCG	TACCGGTAAA	TCTCTTGAGG	AAAACCCCAA	GACCATCAAG	950
AACGGTGACG	CTGCCATGGT	TGTGCTCAAG	CCAATGAAGC	CCATGGTTGT	1000
CGAATCCTTC	ACTGAGTATG	CTCCTCTTGG	TCGTTTCGCT	GTTCGTGAC	1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCGT	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCGC	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCGG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
25	CCCCTTCGCG	TGTCCGCGAT				1070

2) INFORMATION FOR SEQ ID NO: 512

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
 - (B) STRAIN: HM1-IMMS
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTATTAT	GGAAATTCTGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAAGTTTCA	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTATA	CACTCTTGGA	GTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
	TAATCCAGAG	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTTCAGT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGT	ATTGGAAGCTG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

	ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
	ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAATATAT	950
	TAAGAATGGA	GATTTCAGCAC	TTGTTAAGAT	TGTTCCAAC	AAACCACTTT	1000
	GTGTTGAAGA	ATTTGCTAAA	TTCCCACCAT	TGGGAAGATT	TGCTGTTAGA	1050
5	GA					1052

2) INFORMATION FOR SEQ ID NO: 513

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25	GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
	GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
	TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
	GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
	CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
30	TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTACTCGAAG	300
	GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
	CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
	CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
	CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
35	CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
	TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCCGG	600
	ATGAAGGTCG	TCTTCGCCCC	GACGTCCCAG	GTCTCGGAGG	TCAAGTCCGT	650
	CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCCGG	GACAACGTCG	700
	GCTTCAACGT	CCGCGGGCTC	CCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
40	GTCCGGGACG	TGACGAACGA	CCCCCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
	CCAGGTCATC	GTCATGAACC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
	CCGTCAATCGA	CTGCCACACC	GCGCACATCG	CGTGCCAGTT	CCAGCTCTTC	900
	CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCAGATGG	AGAACCCGCC	950
	CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
45	CCCTGTGCTG	CGAGACGTTT	AACGACTACG	CGCCCCCTCG	CCGCTTCGCC	1050
	GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

50 2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

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5  ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG      50
   ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTACAGAT      100
   CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA      150
   CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC      200
10  TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT      250
   TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAGATGG      300
   ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG      350
   GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCCG AGAAGGTGCG      400
   CTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG      450
15  ACAACATGCC GTGGTACAAG GTCCCCACGC TGCTGGACGC GCTCGACATG      500
   CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCCTGCA      550
   GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCCGTG GGGCGCGTGG      600
   AGACCGGCAT CATGAAGCCG GGCAGCTGGT TGACGTTTCG CCCC GCCAAC      650
   GTGACGATG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA      700
20  GGCGCAGCCC GGCGACAACG TCGGCTTCAA CGTGAAGAAC GTGTCCGTGA      750
   AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG      800
   AAGGAGGCGG CCGACTTCAC GGCGCAGGTG ATCGTGCTGA ACCACCCCGG      850
   CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA      900
   TTGCGTGCCG CTTCGCGGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC      950
25  AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT     1000
   CGTGAAGATG GTGCCGAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT     1050
   ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG     1098

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30 2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 1104 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

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   TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACAGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
50  ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
   CTTGAGGCTT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
   TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
55  GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
   GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
   GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCCTGC      550
   AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCCG GGGCCGCGTG      600
   GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA      650
60  CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700

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AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG -750
 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 5 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTC 1104

2) INFORMATION FOR SEQ ID NO: 516

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 25 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 30 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC KCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 35 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 40 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGGCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG 750
 AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 45 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 50 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTCGG 1106

55 2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

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10 TACGCGTG GGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
   ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
15 CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
   TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTG GGCCTGAGG CTACAACCCG GAGAAGGTGC      400
   GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450
20 GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT      500
   GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
   AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG      600
   GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA      650
   CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
25 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
   AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
   GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
   GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
   ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCCG      950
30 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA      1000
   TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC      1050
   TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG      1099

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35

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

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40 (A) LENGTH: 1098 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

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55 TACGCGTG GGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
   ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
   CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
   TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTG GGCCTGAGG CTACAACCCG GAGAAGGTGC      400
60 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450

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	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCCGCCA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTGGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

2) INFORMATION FOR SEQ ID NO: 519

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1071 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
- (B) STRAIN: ATCC 50120

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTACAGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACCGGCAC	GTGCGAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGGCGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGGCGA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
55	GGGCGCTTCG	CTGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 520

- 60 (i) SEQUENCE CHARACTERISTICS:

320

(A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
15	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTCACGATC	ATCGATGCGC	100
	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	TGTGTCTGCA	ACAAGATGGA	CGACAAGACG	300
20	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
25	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
	ATGAAGCCGG	GCGACGTGGT	GACGTTTCGCG	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGTTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
30	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTCGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

55	TCGTTCAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTCGAGTCG	CCCAAGTCGG	100
	TGTTACGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACC GGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTTCGAC	200
	GCAGGGTGGC	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
60	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAAACCCGG	400
	AGAAGGTGCG	CTTCATCCCC	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
	TGCCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTTCGC	650
	GCCCCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	750
10	GTGTGCGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCCG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTGCGAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	CGCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
60	CGTCCG					1106

2) INFORMATION FOR SEQ ID NO: 523

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
20	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
25	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCTTGC	550
30	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
35	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
40	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCG					1105

45 2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

60

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTGCGAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
10	GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGCTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCCG	950
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACGA	TCATCGATGC	GCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTGCGAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGCGGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCGT	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGCTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCCG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGC	CGCAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT		1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C			1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTGCG	AGGCGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCAGACCCGC	GAGCACGCGC	250
TGCTTGCCCTT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCGATCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCGGTGGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAACGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCCGGCGAC	AACGTCGGCT	TCAACGTGAA	GAACGTGTCTG	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	TGAAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGGAGAAGA	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTCAAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

2) INFORMATION FOR SEQ ID NO: 527

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

```

5  GGACRAACTT AAAGCTGAAC GTGAGCGTGG TATCACCATT GATATCTCCC      50
   TGTGGAAATT TGAGACCAGC AAGTACTATG TTACCATCAT TGATGCCCCA      100
   GGACACAGAG ACTTCATCAA AAACATGATT ACAGGCACAT CCCAGGCTGA      150
   CTGTGCTGTC CTGATTGTTG CTGCTGGTGT TGGTGAATTT GAAGCCGGTA      200
   TCTCCAAGAA CGGGCAGACC CGTGAGCATG CCCTTNTGGC TTACACCCTG      250
10  GGTGTGAAAC AACTAATTGT TGGCGTTAAC AAAAKGGATT CCACTGAGCC      300
   ACCCTATAGC CARAAGAGAT ACGARGAAAT TGTTAAGGAA GTCAGCMCCT      350
   AYNTTAAAAA AATTGGYTAC AACCCCGACA CAGTANCATT TGKGCCAATT      400
   TNTGGCTGGA ATGGTGACAA CATGCTGGAN CCAAGTGCTA ATATGCCATG      450
   GTTCAAGGGA TGGAAAGTCM CCCGTAAGGA CGGCAATGCC AGKGAACCM      500
15  CCCTGCTTGA AGCTYTGGAT TGCATTYTGC CACCAAYTTG CCCAACTGAC      550
   AAACCCTTGC GTTTGCCTYT CCAGGATGTC TATAAAATTG GKGGTATTGG      600
   TACTGTCCCT GTGGGTCGTG TGGAGACTGG TGTTCTCAA CCTGGCATGG      650
   TGGTCACCTT TGCTCCAGTC AATGTAACAA CTGAAGTGAA GTCTGTAGAA      700
   ATGCACCATG AAGCATTGAG TGAAGCCCTT CCTGGGGACA ATGTGGGCTT      750
20  CAATGTCAAG AACGTGTCTG TCAAAGATGT CCGTCGTGGC AATGTGGCTG      800
   GTGACAGCAA AAATGATCCA CCCATGGAAG CTGCTGGCTT CACAGCTCAG      850
   GTGATTATTT TGAACCATCC AGGCCAAATC AGTGCTGGAT ATGCACCTGT      900
   GCTGGATTGT CACACAGCTC ACATTGCTTG CAAGTTTGCT GAGCTGAAGG      950
   AGAAGATTGA TCGTCGTTCT GGGAAAAGC TGAAGATGG CCCTAAATTC      1000
25  TTGAAATCTG GTGACGCTGC CATCGTTGAT ATGGTTCCTG GCAAGCCCAT      1050
   GTGTGTCGAG AGCTTCTCTG ATTATCCTCC CCTGGGCCGT TTTGCTGTGC      1100
   GTGAC                                     1105

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30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 935 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Trichomonas vaginalis
   (B) STRAIN: ATCC 30001

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45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

```

   GCACATCCCA GGCTGATGCT GCTATCCTTG TCATCGACTC CACACTCGGT      50
   GGYTTCGAAG CCGGTATCGC TGAACAAGGC CAGACACGTG AACACGCTCT      100
   TCTTGCTTTC AACTCGGCA TCAAGCAGGT CATTGTCGCC GTCAACAAGA      150
50  TGGATGACAA GACAGTCAAC TACAACAAGC CYCGTTTCGA CGAAATCACA      200
   GCCGAAATGA CACGCATCCT TACAGGCATC GGCTACAAGC CAGAAATGTT      250
   CCGCTTCGTC CCAATCTCCG GCTGGGCTGG CGACAACATG ACAGAGAAGT      300
   CTCCAAACAT GCCATGGTAC AATGGCCCAT ACCTTCTTGA AGCCCTCGAT      350
   TCCCTTCAGC CACCAAAGCG CCCATTCGAC AAGCCACTCC GTCTTCCACT      400
55  CCAGGATGTC TACAAGATCA ACGGTATCGG TACAGTTCCA GTCGGCCGTG      450
   TCGAATCCGG CACAATGAAG CCAGGCATGA TCGTTAACTT CGCCCCATCC      500
   ACAGTTACAG CTGAAGTTAA GTCCATCGAA ATGCACCACG AATCCCTTCC      550
   AGAGGCTCTT CCAGGTGACA ACATCGGCTT CAACGTCAAG AACGTTTCCA      600
   CAGCTGATGT CAAGCGTGGC TACGTCGTTG GTGATACAAA GCGTGACCCA      650
60  CCAGTCGAAT GCGCTTCCTT CACAGCTCAR ATGATCATCT CCAACCACCC      700

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	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCCGSCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
	TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTGCGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

2) INFORMATION FOR SEQ ID NO: 529

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
	GAAATTTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GA CTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAGTGCG	500
35	TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
	ACGTGGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCGT	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

50 2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Crithidia rasciculata*
 (B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

```

5   TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA      50
    CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG      100
    CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG      150
    AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG      200
10  CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC      250
    GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCGCCG      300
    AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA      350
    GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT      400
    TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC      450
15  AACGTGGCCA AGGGCCACCG TGGTTTCTCC GTGTTCCGCC GCGTTGGCGA      500
    GCGCACCCGC GAGGGCACCG ATCTGTACCT GGAGATGATG CAGTCGAAGG      550
    TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG      600
    AACGAGCCCC CGGGTGCGCG TCGCGGTGTT GCGCAGTCTG CGCTGACGAT      650
    GGCGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTTCATC      700
20  ACAACATCTT CCGCTTCACC CAGGCCAACT CCGAGGTGTC CGCCCTGCTG      750
    GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT      800
    TGGTATGCTG CAGGAGCGCA TTACGTGCGA GACGAAGGGC TCGATTACGT      850
    CTGTGCAGGC CGTGTACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG      900
    GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT      950
25  TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGCGCGTCGC      1000
    GTATCATGGA CCCCAGATGT ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
    GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
    CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGGTGGACC      1150
    GCGCTCGCAA GGTGACGCGC TTCCTGTCTG AGCCGTTCCA GGTGGCCGAG      1200
30  GTGTTACCG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA      1250
    GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA      1297
  
```

35 2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 1298 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

```

50  CTTCTCGGAG GGCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG      50
    ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC      100
    GCGAACACGG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT      150
    GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
55  GTGAGACGCT GGGCCGCATC TTCAAYGTTT TGGGCGACGC GATCGACCAG      250
    CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
    GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
    AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG      400
    TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
60  CAACGTCGCG AAGGGCCACG GCGGTTTCTC CGTGTGTTGCC GCGGTTGGCC      500
  
```

	AGCGCACGCG	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
5	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTCTG	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTACAG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

20 2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGCCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCGGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTG	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCCTGGAG	TGCGCGTTCG	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTCTG	AGCCGTTCCA	GGTTGCGGAG	1200
60	GTGTTACAGG	GCATGACGGG	CCACTACGTG	CAGCTGGTTC	ACACGGTGGA	1250

GTCTGTTCTCT GGCCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA 1297.

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
 GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGTGCGC GCGCGCGCGT TCGCAGTCT GCGCTGACGA 650
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
 CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
 40 TGGCGGAGTG GGGCATCTAC CTTGCCGTGA ACCCGCTGGA GTGCGCGTCTG 1000
 CGTATCATGG ACCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
 CGCGCGCGCA AGGTGACCCG GTTCTGTGCG CAGCCGTTCC AGGTGCGGA 1200
 45 GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

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5      CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG      50
      ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
      GCGAACACCG GCCGCTGCAT TCGATGCAG ACGACGGACC TGCTGAAGCT      150
      GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10     GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
      CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
      AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
      AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
      TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15     CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG      500
      AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
      GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
      GAACGAGCCC CCGGTGCGC GCGCGCGCGT TCGGCAGTCT GCGCTGACGA      650
      TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
20     GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
      GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
      TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
      TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
      CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25     TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG      1000
      CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
      GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
      CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
      CGCGCGCGCA AGGTGACCCG GTTCTGTGCG CAGCCGTTCC AGGTGCGGA      1200
30     GGTGTTTACG GGCATGACG GCTACTACGT GCAGCTGGCC GACACGGTGG      1250
      AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA      1298
  
```

35 2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 1301 bases
      (B) TYPE: Nucleic acid
40     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```

50     GCATTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
      AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
      GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
      GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55     GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC      250
      CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
      CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
      TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
      CTGTTCCGGC GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
60     CAACAACGTC GCGAAGGGCC ACGGTGTTT CTCCGTGTTT GCCGGCGTTG      500
  
```


	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCAATCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCCGC	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTT	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	GTCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	GCGAGACGCT	GGGTGCGATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTC	CGTGTTTGCT	GGCGTGCGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAG	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTGCGATT	CCTGCCGCCG	TGGGCTACCA	CCCAGCGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTGCA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GAATGTGCTG	GACCGTGCGG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCACT GGCATGACGG GTCACTACGT TCAGCTGGAG GACACGGTGG 1259
 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

5

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
 GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
 25 GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 30 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 CAATGTGCGG AAGGGCCACG GTGGTTTCTC CGTGTGTTGCC GCGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGTTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
 35 TGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700
 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
 40 CGCGACGACG TTCTCGCACC TGGAGTGCAG GACTGTGCTG GACCGCGCGG 950
 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
 45 CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA 1200
 GGTGTTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

50

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACCTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GTTGAAGCTG	150
10	AAGTCGAAGG	TTGTGTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCC	200
	TGAGACGCTG	GGCCGCATCT	TCAACGTGCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGTGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCG	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
15	TTGGTGGCGC	CGGTGTGGGC	AAGACCGTGA	TCATCATGGA	GTTGATTAAAC	450
	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCG	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
20	GGCGGAGTAC	TTCCGAGACG	TGGAGGGCCA	GAATGTGCTG	CTGTTTCATCG	700
	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CGGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	GACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGACGTG	CCTGCGGATG	ATATCACGGA	TCCGGCGCCC	900
25	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
	GGCGGAGTCG	GGGATCTACC	CTGCCGTGAA	CCCCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGTT	ATCGACGAGC	TGACGAGGA	GGACAAGGTC	GTGGTGGACC	1150
30	GCGCGCGCAA	GGTGACCCGG	TTCTGTGCGC	AGCCGTTCCTA	GGTTGCGGAG	1200
	GTGTTACCGG	GATGACGGG	CCACTACGTG	CAGCTGGCCG	ACACGGTGGA	1250
	GTCGTTCTCT	GGGCTGCTGA	TGGGGTCGTA	CGACCAGATC	CCGGAGA	1297

35

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

GTKGAAATGT TCCGCAAGCT GCT

23

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

CGGAARTAGA ACTGSGGACG GTAG

24

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA

23

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

335

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

40

CCRCGICCGG TRATGGTGAA GAT

23

2) INFORMATION FOR SEQ ID NO: 547

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55

GTACAGTTGC TTCAGGACGT ATC

23

60

2) INFORMATION FOR SEQ ID NO: 548

336

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTCGATT TCATCACGTT G 21

15 2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA 24

30 2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG 20

45 2) INFORMATION FOR SEQ ID NO: 551

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

60 GAAGAAAAAA TCTTCGAACT GGCTA 25

2) INFORMATION FOR SEQ ID NO: 552

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

15

TACACGGCCG GTGACTACG

19

20 2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

35

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCTTACA TCGTTGTTTT TCTC

24

50

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA 24

2) INFORMATION FOR SEQ ID NO: 556

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

20

CGGCGCNATC YTS GTTGTTG C 21

25 2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG 22

40

2) INFORMATION FOR SEQ ID NO: 558

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYG CITGGGT 20

55

2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

CCGACRGCRA YIGTYTGICK CAT

23

2) INFORMATION FOR SEQ ID NO: 560

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC

23

2) INFORMATION FOR SEQ ID NO: 561

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40

ACIGTICGGC CRCCCTCACG GAT

23

2) INFORMATION FOR SEQ ID NO: 562

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

55

CARATGRAYG ARCCICCI GG IGYIMGIATG

30

60

2) INFORMATION FOR SEQ ID NO: 563

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT

26

15

2) INFORMATION FOR SEQ ID NO: 564

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA

29

30

2) INFORMATION FOR SEQ ID NO: 565

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

45 GGYTGRTAIC CIACIGCIGA IGGDAT

26

2) INFORMATION FOR SEQ ID NO: 566

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

60

5 2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

20.

2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35

2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT

23

50

2) INFORMATION FOR SEQ ID NO: 570

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT 23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT 23

2) INFORMATION FOR SEQ ID NO: 572

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

35

RTIRTIGGIS CIGTIRTIGA 20

2) INFORMATION FOR SEQ ID NO: 573

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC 20

2) INFORMATION FOR SEQ ID NO: 574

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

343

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG 23

2) INFORMATION FOR SEQ ID NO: 575

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GTAA 25

2) INFORMATION FOR SEQ ID NO: 576

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40 AACTTCRTCA AGAAGGTYGG TTACAA 26

45 2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA 20

60

2) INFORMATION FOR SEQ ID NO: 578

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA 20

2) INFORMATION FOR SEQ ID NO: 579

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA 20

2) INFORMATION FOR SEQ ID NO: 580

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC 25

2) INFORMATION FOR SEQ ID NO: 581

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

5 2) INFORMATION FOR SEQ ID NO: 582

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

20

2) INFORMATION FOR SEQ ID NO: 583

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

35

2) INFORMATION FOR SEQ ID NO: 584

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

50

2) INFORMATION FOR SEQ ID NO: 585

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG 20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA 20

25 2) INFORMATION FOR SEQ ID NO: 587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

CGTATTATCA AAAGACGAAG 20

40

2) INFORMATION FOR SEQ ID NO: 588

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA 20

55

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40

TCCTGGTTCT ATTACACCAC

20

45 2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

55

CAAAGCTGAA GTATACGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCCTAACT ATCGCCACA 20

15

2) INFORMATION FOR SEQ ID NO: 594

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC 20

30

2) INFORMATION FOR SEQ ID NO: 595 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

TTAAAGCAGA CGTATACGTT 20

45

2) INFORMATION FOR SEQ ID NO: 596

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

60

5 2) INFORMATION FOR SEQ ID NO: 597

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

20

2) INFORMATION FOR SEQ ID NO: 598

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

35

2) INFORMATION FOR SEQ ID NO: 599

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

20

50

2) INFORMATION FOR SEQ ID NO: 600

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

350

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA 20

2) INFORMATION FOR SEQ ID NO: 601

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

20

GTTTCACGTG ATGATGTACA 20

25 2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTGGTATT 20

40

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC 20

55

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

351

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

10 GGTGATGAAG TAGAAATCGT 20

2) INFORMATION FOR SEQ ID NO: 605

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT 20

2) INFORMATION FOR SEQ ID NO: 606

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40 ATTAGACTAC GCTGAAGCTG 20

45 2) INFORMATION FOR SEQ ID NO: 607

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

60

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	58
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTT	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACATCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20

2) INFORMATION FOR SEQ ID NO: 608

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: ATCC 19434

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACATC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTCCCTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCCCTG	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACCTGA	750
	A					751

55

2) INFORMATION FOR SEQ ID NO: 609

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid

60

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
15	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTCTG	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
20	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
25	AAGGTGGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae* Rd
(B) STRAIN: KW20
(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAACTCG	TGAACACATC	TTATTAGGTC	100
50	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAAC	200
	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCACTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
55	TGACCAACCG	TTCCTTCTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAGAAC	GAGGTATTAT	CCGTACAGGT	450
	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAACGTGGT	600
60	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650

	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATCTCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTGGT	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 611

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCATAACT	ATCGCCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACTGG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GTTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TGCCTATCGA	AGACGGAA				818

45 2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

60

355

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTTG	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAACTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 778 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: ATCC 33105

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTG	CGTTCCTTTC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTCGCGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTCGATTC	AGAAGTGATC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 653 bases

356

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTTAAGCACT	TGATCGTTTT	100
15	CTTGAACAAA	GTAATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TTAAAGGTTT	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350
20	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCATCA	600
25	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45	CCATTCTAGT	TGTATCTGCA	ACAGATGGAC	CAATGCCACA	AACACGTGAA	50
	CATATTTTAT	TGTCACGTCA	AGTAGGTGTT	AAATATTTGA	TCGTCTTCTT	100
	GAACAAAATC	GACTTAGTAG	ATGATGAAGA	ATTGATTGAT	CTTGTCGAAA	150
	TGGAAGTTCG	TGAATTATTA	AGCGAATATG	GTTTCCCAGG	TGACGATACA	200
50	CCAGTCATCA	AAGGTTTCAGC	ATTAAAAGCT	TTACAAGGAG	ATCCTGATGC	250
	AGAAGCAGCT	ATCATGGAAT	TGATGGATAC	TGTTGATGAA	TATATCCCAA	300
	CACCAGAACG	TGATACAGAC	AAACCATTAT	TGTTACCACT	GGAAGATGTC	350
	TTCTCAATCA	CAGGTCGTGG	GACTGTTGCT	TCAGGTCGTA	TCGATCGTGG	400
	TGCAGTTCGT	GTAAGTGATG	AAATCGAAAT	CGTCGGTATC	AAACCTGAAA	450
55	CACAAAAAGC	TGTTGTAACT	GGGGTCGAAA	TGTTCCGCAA	GACATTAGAC	500
	TATGGTGAAG	CAGGAGATAA	CGTTGGGGTA	TTGTTACGTG	GTATCCAACG	550
	TGAAGATATC	GAACGTGGAC	AAGTAATCGC	AAAACCAGGT	TCAATCACAC	600
	CACATACAAA	ATTCAAAGCA	GAAGTGATCG	TATTGACAAA	AGAAGAAGGT	650
	GGACGTCATA	CACCATTCTT	CAATAACTAT	CGTCCACAAT	TCTACTTCCG	700
60	TACAACTGAC	GTAAGTGAA	CAATCGTTTT	ACCTGGAGGC	ACTGAAATGG	750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCAGTT 800
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG 50
TGAACATATC TTGTTATCAC GTCAAGTAGG GGTTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTTA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
25 GAAATGGAAG TTCGGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
30 GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT 500
GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCTATTA CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAGTT TATGTATTGA CGAAAGAAGA 650
35 AGGTGGCCGT CATACGCCA 669

2) INFORMATION FOR SEQ ID NO: 617

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC 50
GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTTAATCGTC 100
TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAAC TAGT 150
TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTT CCTGGCGATG 200
ATATTCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA 250
60 GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT 300

358

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGGGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTT	CGTAAACTT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

15 2) INFORMATION FOR SEQ ID NO: 618

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAACTCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AAC TGGACTT	GAAATGTTCC	GTAAAACCTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
45	AGGTGGACGT	CATACACCAT	CTT			673

2) INFORMATION FOR SEQ ID NO: 619

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 60 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

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5   TTTTCATATTT TTAAGGATTT TGTTTTAGCA CCCATCCGAC CTCAGTCAAT    50
    ATATCCTTTC GCGACCAGGC TTTCTCCCT TTTGCTGCTA ACTGGTTACA    100
    GATTTTCCTA TTTTGGTCA TTTTATCTT TGAAACTGAT TAAGCTGAAA    150
    AAATTTGAGC TTCTTTGTTG TAAACTATTT TGTGCTTTCA GTTTATTCT    200
    AGCTCGACAA AGGTAACAGA CAAAAATGTC AGCTTTATTA CCAAGATTAC    250
    TCACAAGAAC AGCTTTTAAA GCTTCTGGGA AACTTCTGAG GCTCTCTTCA    300
10  GTAATTTCTA GGACCTTTTC TCAAACACT ACTTCCTATG CAGCTGCTTT    350
    TGATCGTTCC AAACCGCATG TAAATATAGG TACGATCGGC CATGTTGATC    400
    ATGGGAAGAC AACTTTAACC GCAGCCATTA CGAAAACGTT AGCCGCAAAA    450
    GGTGGTGCCA ACTTCTTGGA CTATGCTGCC ATCGATAAGG CTCCGGAAGA    500
    AAGAGCTCGT GGTATTACAA TTTCTACTGC ACACGTGGAA TACGAAACGG    550
15  CCAAGAGACA TTATTCTCAC GTCGACTGTC CAGGCCACGC TGATTACATC    600
    AAGAATATGA TTACCGGTGC TGCTCAAATG GATGGTGCTA TCATTGTTGT    650
    AGCTGCTACC GATGGACAAA TGCCCCAAAC TAGAGAACAT TTACTTTTGG    700
    CCAGACAAGT TGGTGTCCAA CATATTGTCG TTTTGTGTTA CAAGGTTGAT    750
    ACCATTGATG ATCCAGAAAT GTTAGAGTTA GTCGAAATGG AAATGAGAGA    800
20  ACTTTTAAAC GAATATGGGT TTGACGGTGA TAATGCTCCA ATTATCATGG    850
    GTTCTGCCCT TTGCGCTTTG GAAGGTCGCC AACCTGAAAT TGGGGAGCAG    900
    GCCATCATGA AACTTTTGGA TGCAGTGGAT GAGTATATTC CTACACCTGA    950
    AAGAGATTTG AACAAGCCTT TCTTGATGCC CGTTGAAGAT ATCTTCTCTA   1000
    TCTCCGGTAG AGGTACTGTG GTCAGTGGTC GTGTGGAAAG GGGTAATTTA   1050
25  AAGAAAGGTG AGGAATTGGA AATTGTTGGT CACAACCTCA CCCCATTGAA   1100
    AACAACAGTT ACTGGTATTG AAATGTTTAG AAAGGAATTG GACTCTGCTA   1150
    TGGCAGGTGA CAATGCCGGT GTTTTACTTA GAGGTATCAG GAGAGATCAA   1200
    TTGAAGAGAG GTATGGTCTT AGCTAAGCCA GGTACCGTTA AAGCCCATAC   1250
    AAAGATTCTA GCCTCTTTGT ACATTTTATC CAAAGAGGAA GGTGGTAGAC   1300
30  ATTCTGGGTT TGGTGAAAAC TACAGACCAC AAATGTTTAT AAGAACAGCT   1350
    GATGTTACAG TTGTGATGAG ATTTCCCTAAG GAGGTGAAG ATCATTCTAT   1400
    GCAAGTTATG CCAGGTGACA ATGTTGAAAT GGAATGTGAT TTGATCCATC   1450
    CTACCCCATT AGAAGTTGGT CAACGTTTCA ATATCAGAGA GGGTGGAAGA   1500
    ACTGTTGGTA CCGGTCTAAT CACACGTATT ATTGAATAGA CTTATTGATG   1550
35  CAACTGGAGT ATATTTCTAT ATATTCTGTT CATTTCCCCT CTCATAATAT   1600
    ATAATTGTTT CGTTAAAATT TTATACGTGT AAATAAAGTG CCATAAATTT   1650
    TTCAGCTTTA CTTTTGGTAG AGTCCTGCTA GCACTAGATT TTACAATTTT   1700
    ATGTGCACAC ACC                                     1713

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2) INFORMATION FOR SEQ ID NO: 620

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45  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

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50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

55 ATTGGTGCAT TGCTACGT

18

2) INFORMATION FOR SEQ ID NO: 621

60 (i) SEQUENCE CHARACTERISTICS:

360

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

15 TGGTGCAATC TTAGTTGTTT CTGCAACTGA CGGTCCGATG CCTCAAACAC 50
 GTGAACACAT TTTATTGTCA CGCCAAGTTG GTGTAAAATA CCTGATTGTT 100
 TTCTTGAACA AAGTTGATTT AGTCGATGAT GAAGAATTGA TCGATTGTTG 150
 AGAAATGGAA GTTCGCGAGT TATTGAGCGA ATATGGTTTC CCAGGCGATG 200
 ACACTCCTGT GATCAAAGGT TCCGCATTAA AAGCATTGCA AGGCGATCCA 250
 GATGCTGAAG CTGCTATTAT GGAATTGATG GATACAGTAG ATGAATATAT 300
 20 CCCAACACCA GAACGTGATA CAGATAAACC ATTACTATTG CCAGTGGAAG 350
 ACGTCTTCTC AATTACAGGT CGAGGAACTG TTGCCTCAGG TCGTATTGAT 400
 CGTGGTGCTG TTCGTGTCGG TGATGAGGTA GAGATCGTAG GGATCAAACC 450
 TGAAACACAA AAAGCAGTTG TAACAGGTGT AGAAATGTTT CGTAAAACGT 500
 TAGATTACGG GGAAGCTGGG GATAACGTAG GCGTGTGTTT ACGGGGGATC 550
 25 CAACGTGACG ATATCGAACG TGGACAACTA CTTGCTAAAC CAGGTTCCAT 600
 TACTCCACAT ACAAATTTCA AAGCAGAAGT GTACGTGTTG ACAAAGAAG 650
 AAGGTGGACG TCATACTCCA TTCTTCAACA ACTATCGTCC ACAGTTCTAC 700
 TTCCGCACAA CTGATGTTAC AGGAACAATC ACATTGCCAG AAGATACAGA 750
 A 751

30

2) INFORMATION FOR SEQ ID NO: 622

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

50 GTCAAATGGG ACGAATCCAG ATTCCAAGAA ATTGTCAAGG AAACCTCCAA 50
 CTTTATCAAG AAGGTTGGTT ACAACCCAAA GACTGTTCCA TTCGTCCCAA 100
 TCTCTGGTTG GAACGGTGAC AACATGATTG AAGCTACCAC CAACGTTCCA 150
 TGGTACAAGG GTTGGGAAAA GGAAACCAAG GCCGGTGTCTG TCAAGGGTAA 200
 GACTTTGTTG GAAGCCATTG ACGCCATTGA ACAACCATTCT AGACCAACTG 250
 ACAAGCCATT GAGATTGCCA TTGCAAGATG TTTACAAGAT TGGTGGTATT 300
 55 GGTACTGTGC CAGTCGGTAG AGTTGAAACC GGTGTCATCA AGCCAGGTAT 350
 GGTTGTTACT TTCGCCCCAG CTGGTGTTAC CACTGAAGTC AAGTCCGTTG 400
 AAATGCATCA CGAACAATTG GAACAAGGTG TTCCAGGTGA CAACGTTGGT 450
 TTCAACGTCA AGAACGTTT CGTTAAGGAA ATCAGAAGAG GTAACGTCTG 500
 TGGTGACGCT AAGAACGATC CACCAAAGGG TTGCGCTTCT TTCAACGCTA 550
 60 CCGTCATTGT TTTGAACCAT CCAGGTCAAA TCTCTGCTGG TTACTCTCCA 600

TTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCTG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

2) INFORMATION FOR SEQ ID NO:623

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 1269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: ATCC 44104

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
25 CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTCAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
30 CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCTTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCCCTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTACACT	GCCCGTAAGC	CTGACCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTGATTTCGC	CGTCCGAGA				1269

50

2) INFORMATION FOR SEQ ID NO: 624

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 753
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: Genomic DNA

362

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 36801

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTTCGTT	100
10	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCAACA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
15	TATGGTTGTT	ACTTTCGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAAA	GGGTTGTGAC	TCTTTCAATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
20	CCAGTCTTGG	ATTGTACACC	TGCCACATT	GCTTGTAAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAATGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	750
	CCA					753

25

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

	CGTTGAAGAC	ACGACCCAAA	GTATCC	26
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40

2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

55	TACCACCTTT	TAAGTAAGGT	GCTAAT	26
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60

2) INFORMATION FOR SEQ ID NO: 627

364

2) INFORMATION FOR SEQ ID NO: 631

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

15 CAGACCAACY GAIAARCCAT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 632

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

30

CCCTTTGGTG GRTCSTKCTT GGA

23

35 2) INFORMATION FOR SEQ ID NO: 633

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT

26

50

2) INFORMATION FOR SEQ ID NO: 634

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRCIATTGC YATGGA

26

5

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

20 AAACCRGTIA RRGCRCTCT IGCTCT

26

2) INFORMATION FOR SEQ ID NO: 636

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 637

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50

ACGTCAGTIG TACGGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 638

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT 26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTTCWACAC CWGTIACA 28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA 23

40

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG 26

60

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642
GGCGTIGGIG ARCGIACICG TGA

15 2) INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643
ACTGGIGTIG ARATGTTCCG YAA

30 2) INFORMATION FOR SEQ ID NO: 644

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644
ACGTCIGTIG TICKGAARTA GAA

45

2) INFORMATION FOR SEQ ID NO: 645

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645
ACGTCIGTIG TICKGAARTA RAA

60

2) INFORMATION FOR SEQ ID NO: 646

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

15 ATCGACAAGC CITTCTTIAT GSC

23

2) INFORMATION FOR SEQ ID NO: 647

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

30 ACGTCCGTSG TRCGGAAGTA GAACTG

26

35 2) INFORMATION FOR SEQ ID NO: 648

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG

26

50 2) INFORMATION FOR SEQ ID NO: 649

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

5

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

20 TTACGGAACA TYTCAACACC IGT

23

2) INFORMATION FOR SEQ ID NO: 651

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA

25

2) INFORMATION FOR SEQ ID NO: 652

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

50

CCWAYAGTIY KICCICCYTC YCTIATA

27

2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT 20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG 20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucléic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA 20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA 22

2) INFORMATION FOR SEQ ID NO: 657

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657
10 TTGTCCACGT TCGATRTCTT CA 22

15 2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658
 GATYTAGTCG ATGATGAAGA ATT 23

30 2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659
 GCTTTTTGIG TTTCWGGTTT RAT 23

45 2) INFORMATION FOR SEQ ID NO: 660

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660
 GTAGAATTGA GGACGGTAGT TAG 23

60

2) INFORMATION FOR SEQ ID NO: 661

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

15 GTAGAAATGT GGWCGATART TRT

23

2) INFORMATION FOR SEQ ID NO: 662

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC	50
	GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT	100
	GCTCTGAACA AGTGCGACAT GGTTGATGAT GAGGAAATCA TCGAGCTCGT	150
	CGAGATGGAG ATCCRTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG	200
	CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG	250
40	TGGACCCAGT CCATCATCGA CCTCATGCAG CTTTGCKATG ATTCCATCCC	300
	AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA	350
	TCTTACCATT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT	400
	GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA	450
	KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG	500
45	ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG	550
	CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
	CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG	650
	GTGGCCGCCA CACCCCATTC TTCGACAACT ACCGCCCACA GTTCTACTTC	700
	CGCACCACCG ACGTTACCGG TGTTGTGAAG CTTCTGAGG GCACCGAGAT	750
50	GGTCATGCCT GGCGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG	800
	TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC	832

55 2) INFORMATION FOR SEQ ID NO: 663

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

373

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

```

10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA      50
   CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA      100
   CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT      150
   ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG      200
15 TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT      250
   TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT      300
   GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG      350
   TGGTGCCGGT GTCGGTAAGA CCGTGTTTCA CCAGGAGTTG ATTAACAACA      400
   TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT      450
20 ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT      500
   CAACTTGGAG GGCGACTCCA AGGTGGCCTT GGTGTTCCGG CAGATGAACG      550
   AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC      600
   GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA      650
   CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC      700
25 GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT      750
   TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT      800
   GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCGCCA      850
   CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC      900
   GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT      950
30 GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG      1000
   TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT      1050
   TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC      1100
   CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTGCTGTC GCCGAGGTTT      1150
   TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG              1192
35

```

2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

```

10 ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
   TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
   TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
   AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
   AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
15 AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
   AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
   TGGTGGTGTG GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
   GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
   GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
20 AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
   AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
   GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTTGGGAAA AGGAAACCAA      650
   GGCCGGTGTG GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
   AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
25 GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
   CCGTGTTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA      850
   CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
   GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
   AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
30 GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
   ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC      1100
   TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
   AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
   AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
35 ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG      1300
   GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG      1350
   GCTGCTCAAA AGGCTGCTAA GAAATAA      1377

```

40

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

```

ATGGTTTTGC CAAGACTATA TACTGCTACA TCCCGTGCTG CTTTTAAAGC      50
AGCCAAACAA TCCGCTCCGC TTCTATCCAC TTCGTGGAAA AGATGTATGG      100
CCTCAGCTGC TCAATCTACT CCAATCACCG GTAAAGTTAC CGCTGTCATT      150
60 GGTGCCATTG TTGACGTTCA TTTTGAACAA TCAGAGTTGC CCGCTATTTT      200

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	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGT	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCT	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCT	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCAGAA	GGTATTTTCT	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCT	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

30

2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1293 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: Y

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCCGGAG	200
	ACACTTGGCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTTTG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAATT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGACTCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCTAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCGG	AGA	1293

15

2) INFORMATION FOR SEQ ID NO: 668

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Corynebacterium glutamicum*
- (C) ACCESSION NUMBER: X77034

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTCT	TGAAGTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTA	TGCCTATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCT	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTT	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTGCAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTCGCT	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCGT	GTCACCAAGA	TCATCAAGTA	A	1191

60

2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

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15  ATGGCTACTG GAAAGATTGT CCAGGTAATC GCGCGCGTAG TTGACGTCGA      50
    ATCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA      100
    ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT      150
    ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT      200
    GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAAGCGA      250
20  CTCTGGGCCG TATCATGAAC GTACTGGGTG AACC GGTCGA CATGAAAGGC      300
    GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA      350
    CGAAGAGCTG TCAAACTCTC AGGAACTGCT GGAACCCGGT ATCAAAGTTA      400
    TCGACCTGAT GTGTCCGTTC GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT      450
    GGTGCGGGTG TAGGTAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT      500
25  CGCGATCGAG CACTCCGGTT ACTCTGTGTT TCGGGGCGTA GGTGAACGTA      550
    CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC      600
    GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG      650
    TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG      700
    AAGTCCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG      750
30  GCGGTACCGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG      800
    TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA      850
    CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT      900
    GCGGATGACT TGACTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA      950
    CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG      1000
35  CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT      1050
    GGTCAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG      1100
    TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT      1150
    CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC      1200
    CTGTCCCAGC CGTTCTTCGT GGCAGAACTA TTCACCGGTT CTCCGGGTAA      1250
40  ATACGTCTCC CTGAAAGACA CCACTCCGTG CTTTAAAGGC ATCATGGAAG      1300
    GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC      1350
    GAAGAAGCTG TGGAAAAAGC CAAAAAACTT TAA                          1383

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2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: NCTC 11638
 (C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTACAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTGCGT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTCACAG	350
10	AAAAGCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCTG	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCAT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	GCGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCTCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTCA	AGAGGTTTAA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

35 2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
 (B) STRAIN: DSM 792
 (C) ACCESSION NUMBER: extracted from AF101055

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTTACAG	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AAACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAAGTTG	250
	GAGAAAATGT	TTTAGGACGT	CTTTTTAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGGTGG	AAAAATCGGT	450

	TTGTTCCGGTG	GTGCCCGGTGT	TGGTAAACAA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CACTTGCAAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTCTTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTTG	1150
15	ATGAACTTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAATGA	TGGAAAGCTA	1400
20	A					1401

2) INFORMATION FOR SEQ ID NO: 672

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Cytophaga lytica*
- (B) STRAIN: DSM 2039
- (C) ACCESSION NUMBER: M22535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

40

	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TCTTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCAACTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAACTCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

15 2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
 (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTCAGGA	150
	AATCCAATTC	AGGTTCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGG	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAAGTC	GTGAAGGTAA	500
	TGACTTGTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTC	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGGTTCT	ATAACATCT				819

50

2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

	AGAGCGAAGT	ACCAAGTGT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
	GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
	CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
10	AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
	CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
	CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
	AGTCTAGTGC	AACTGAACTT	TTGGAAACGG	GTGTTAAGGT	TATCGACCTG	350
	ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTCG	GTGGTGCGGG	400
15	TGTAGGTAAG	ACCGTTAACA	TGATGGAACT	TATCAACAAC	ATCGCGCTAC	450
	AGCACTCAGG	TTTGTCTAGT	TTTGTCTGGG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
	ACAACCGAA	CTGTCGAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
	CACCAGGCAA	CCGTCTGCGT	GTAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
20	AAGTTCCGTG	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
	CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
	CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
	CAAGAACGTA	TCACGTCAAC	CAAAAAAGGT	TCTATCACCT		840

25

2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

	CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100
45	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTCGTGAGC	TGCTGTCTGA	GTACGATTTC	CCAGGTGATG	200
	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
	TCCAGAGCCA	GAGCGTGCG	TAGACATGGC	ATTCCTGATG	CCAATCGAAG	350
50	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACTRCTACG	TGGTACTAAG	550
	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
55	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
60	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

2) INFORMATION FOR SEQ ID NO: 676

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania enriettii*
 15 (B) STRAIN: ATCC 50120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

	CTTCTCGGAT	GCGTGCCGC	CGGTGCTGAC	GCGCTGGAC	GTGACGGAGG	50
20	AACTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
25	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTCGCC	GGCGTTGGGG	500
	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
30	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
	GGGCCGCATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
35	TCGGCATGTT	GCAGGAGCGC	ATCACGTCGA	CGACGAAGGG	GTGATCACAG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCCGCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCC GCGGTCA	ACCCACTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
40	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTGTGCA	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
45	AGTCGTTCTC	CGGTTTGCTG	ATGGGGTCGT	ACGACCAGAT	TCCGAGAGA	1298

2) INFORMATION FOR SEQ ID NO: 677

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia microtti*
 60 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGTAT	TACTATTGAC	ATTACTCTCT	50
5	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCACATT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

2) INFORMATION FOR SEQ ID NO: 678

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: Lev-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGCCCTG	ACTAAACTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTACTTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCCGATT	CACCCAGGCC	GGTTCCGAGG	TGTCTGCCTT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

60 2) INFORMATION FOR SEQ ID NO: 679

384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

15 TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT 50
 ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG 100
 TACCACGAAA TGAGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA 150
 GGTCGCTCTT GGTGAGTTCT TTTTTTTGGG AGCTAATTAG TCGATGACGT 200
 20 GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC 250
 CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT 300
 ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT 350
 TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT 400
 CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA 450
 25 TGCAAGAGCG AATGTAAGTT GCATTTTTTTG TGATTTTACG GCAAGTCTTG 500
 ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG 550
 TC 552

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2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

50 TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC 50
 GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT 100
 ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTGTAGAT GATCATAAAT 150
 AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT 200
 AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT 250
 TTTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC 300
 CTTTTTTTATA AAATTAATCA GGTCTTGTC GTGGTCAAAA GGTTGTTGAT 350
 ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT 400
 55 CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA 450
 AGTCTCACCG TGCTATTAC GCTGAAGCTC CAGAATTCGT TGATCAATCT 500
 CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC 550
 TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCGGTGGT GCTGGTGTAG 600
 GTAAACTGT CTTGATTCAA GAACCTATTA ACAACATTGC TAAAGCCCAT 650
 60 GGTGGTTACT CTATTTTCTG TGGTGTGGT GAACGTACTC GTGAAGGTAA 700

CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
CGTGCCCGTG	TTGCTTTAAC	TGGTTTAAAC	ATTGCTGAAT	ACTTCCGTGA	850
TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5 CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
TATTACTACT	ACCAAGAA				1018

10

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

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2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

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2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

55 GTIACIGGIT CISWIAWRTC ICCICC

26

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2) INFORMATION FOR SEQ ID NO: 684

386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
(C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
30	GGTACTACTT	TATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTGA	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCCTGTTT	CTGCTGATCA	TAACTTATC	TTGAAAATA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTTACTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAACTCA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTCA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTTCA	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCTCAACA	TATGCTGTTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTCT	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTT	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAG	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTT	TGGGGGTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAATA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAAC	CACTATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

2) INFORMATION FOR SEQ ID NO: 685

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Enterococcus hirae*
- (B) STRAIN: ATCC 9790
- (C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

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	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCGAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTGG	GTACGTGGAT	GAAACGAAGA	TCATTGAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCG	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCGGT	700
55	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTT	CTGAACTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCAGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGGA	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAACTGG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCTT	GAAGTAGCAA	AATCGATTCG	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

20 2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029
 (C) ACCESSION NUMBER: Genome project

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCAG	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTCGA	GGAGCTCTTG	TTACGTTTTTC	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTT	250
	TCGATGGACT	TCAAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTTC	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCCT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTCCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTGCT	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCCTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTCCAGA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCACTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTTG	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTCC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

15

2) INFORMATION FOR SEQ ID NO: 687

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1758 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Halobacterium salinarum*
- (C) ACCESSION NUMBER: S56356

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTCG	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
	CCAGCCCCTC	GACAACACGG	GCGAACCGCT	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TCGACGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTGCG	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGCCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCAGAA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCCGTTG	CCGGGCGTGA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCGGCG	AGGAGGGGTA	TCCCGCGTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTCAC	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTCGACA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

	CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1800
	TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCCGCCGA	1550
	GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
	TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5	GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGACG	ACGAGCACGA	1700
	GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
	TCTACTGA					1758

10

2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
 (C) ACCESSION NUMBER: L09234

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

	GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
	GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
30	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
	GAAGTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
35	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
	AGTGGGACTT	CAGTCCCGTC	AGTGTCAAGG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGCTGCCG	CCCCGTGCCA	AGGGAAGTGT	CACGTACATT	GCAGAACCTG	600
	GAAACTACAC	GATTGATGAT	GTTGTCTCTG	AGACAGAATT	TGACGGCGAG	650
40	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCCAGGCC	700
	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
	GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
	CTCAAACCTC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
45	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCTGT	GGAGATTGAT	950
	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000
	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
	TCAAATTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
50	TGAAATCCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
55	TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
	CAAGAATTTT	CCAGAGTTTG	TCCCACTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
	GGATGATTTT	CTGCAACAGA	ACAGCTATTC	ACCATATGAC	CGTTTCTGCC	1650
60	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700

	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAGATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTGAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTGAG	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCCG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTT	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTT	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTTCG	2500
	ACCTCACATT	GTAATCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAATGG	TGAATGTATT	TTATATTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCTTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTAT	TAGCATTTCA	CTGTTGTCAC	3100
	ATAAATTATG	CCCGGAAT				3118
30						

2) INFORMATION FOR SEQ ID NO: 689

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plasmodium falciparum*
 (B) STRAIN: 3D7
 (C) ACCESSION NUMBER: L08200

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAACT	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTCGTGA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCT	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTGGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCTCTG	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	TTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTAGCT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACTAC	1250
15	AGCAACCATG	TCTATTGTTT	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTCTTT	1400
	ATCTTTAAGA	CAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAGTATT	TAAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

30 2) INFORMATION FOR SEQ ID NO: 690

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3216 bases
- (B) TYPE: Nucleic acid
- 35 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
- (B) STRAIN: X2180-1A
- (C) ACCESSION NUMBER: J05409

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTGCTT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTT	ACTCTTTACC	ATACTTGGCC	650
60	TGTTCTGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTGCAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAG	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGGTAA	TGGTATTCGC	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAAT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCT	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGCTCTG	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACTTATGAT	GCTTTCTGTC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1860 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

```

ATGGCGGGAG GAATTGAACT GGCCAAGAAG GCTATCAGGA GCCTCAAAAA 50
TTACGACGAG CATGAAAACC GATATGGATC TATTTTCAGC GTTCTGGGTC 100
CTGTCGTTGT TGCAGCCAAT ATGCTTGGAT GTTCGATGTA CGAACTCGTT 150
15 CGCGTTGGTC ATGAAGAACT AGTTGGTGAA GTAATTCGTA TCCATCAAGA 200
TAAATGTACT ATTCAAGTAT ACGAAGAGAC GTCCGGTCTC ACTGTTGGTG 250
ATCCTGTCCA ACGCACTGGA AAGCCATTAT CTGTTGAATT AGGTCCTGGT 300
TTAGCTGAGA CTATTTATGA TGGTATCCAA CGTCCGTTAA AGCAAATTTT 350
CGACAAATCT CAAAGTATTT ATATTCCTAG AGGTATTAAT ACAGAATCAC 400
20 TTAATCGTGA GCATAAGTGG GATTTACAC CAAATAAGGA TTTACGCATT 450
GGCGATCATG TATCCGGTGG TGATGTTTTT GGTTCTGTAT TTGAAAACCTC 500
TCTTTTCAAT GATCATAAAA TTATGTTACC CCCTAGAGCC CGTGGTACCG 550
TCACATATAT TGCTGAAGCT GGATCATACC ATGTTGATGA AAAACTTCTT 600
GAAGTCGAGT TTAATGGCAA GAAACATTCT TTTAGTATGT TGCATACTTG 650
25 GCCTGTCCGT GCTGCTCGTC CAGTTGCGGA CAACTTAACT GCTAATCAAC 700
CTTTATTGAC TGGTCAACGT GTTTTGGATG CGTTATACCC CTGTGTTCAA 750
GGTGGCACTA CTGCTATCCC CGGTGCCTTT GGTTGTGGTA AAACAGTTAT 800
TTCACAATCT CTTTCTAAGT ACTCTAATTG TGATTTGATT GTTTACGTCG 850
GTTTGGTGTA ACGTGGAAC GAAATGGCAG AAGTGTTAAT GGATTTCCCA 900
30 GAACCTAACAA TTGATATTAA TGGTAAACCA GAGCCCATTA TGAAGCGTAC 950
TACATTGGTA GCCAACACTT CTAACATGCC TGTCGCTGCT CGTGAAGCTT 1000
CCATTTATAC CGGTATTACA CTTGCTGAAT ATTATCGTGA TCAAGGTAAG 1050
AACGTTTCAA TGATGGCTGA TTCTACATCT CGTTGGGCTG AAGCTTTGCG 1100
TGAAATTTCT GGTCGTTTGG CTGAGATGCC TGCCGATTCT GGTTATCCCG 1150
35 CTTATTTGGG TGCCAAATTG GCTTCTTTTT ACGAACGTGC TGGTCGTGCT 1200
CGTTGCTTGG GAAGTCCTGA CCGTGAAGGA ACAGTTTCAA TTGTTGGAGC 1250
TGTTTCTCCT CCGGGTGGTG ATTTTCTGTA TCCTGTTACT AGTGCAACCT 1300
TGGGAATTGT TCAAGTCTTC TGGGGTTTGG ACAAGAAATT GGCCCAACGT 1350
AAACACTTTC CCTCAATCAA CACCTCTCTT TCCTATTCTA AATACATCAA 1400
40 TGCTTTGCAA CCTTGGTATG AGGAAAGAT TCCAGGCTTT AATACTCTTC 1450
GTGATCAAAT CAAACAGATC ATTCAACAAG AAGATTCCAT GTTGGAATTT 1500
ATTCAGTTGG TTGGTAAGTC GGCTCTTTCT GAAACGGATA AAGTTACTTT 1550
GGACATAGCC GGTATTATTA AGAATGACTT CTTACAACAA AACGGTTATT 1600
CTGATTACGA TCGCTGTTGC CCTCTTTACA AGACTTATCA TATGATGCGA 1650
45 AACATGATTG CTTACTACAC AAAGGCTAAA AGTGCCGTG AAAGTGGTAG 1700
CGTTCCTTGG TCAAAGATTA AAGAAAGTAC TTCAGATATC TTTTATGAGT 1750
TAACCTCGAT GAAATTCGAA AACCCTAATG AAGGCGAGAA GGAAATAGTC 1800
GAACACTATG AAATCTGCA CAAGAAGATT GAGGACAAGT TTCACACTCT 1850
50 GACTGAGTAA 1860

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2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

```

10 ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
   GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG      100
   CTATGTATGA GCTTGTGCAG GTAGGTTCTT TCCGGTTAGT GGGCGAGATC      150
   ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
   TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTTCGC      250
15 TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
   CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG      350
   CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTTAAGCCAT      400
   GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
   GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT      500
20 GCGGGGCCGT GTTACTTCCA TTGTTCTTTC AGGAAATTAC ACCCTCCAAG      550
   ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAACTTT      600
   ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
   CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
   CATCCGTCCA GGGTGGAAACA TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
25 AAGACGGTTA TCAGTCAGGC TCTTTTCGAAG TTCTCCAACA GCGACGCTGT      800
   TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
   TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
   ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC      950
   TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCTGT      1000
30 ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT      1050
   GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG      1100
   TGGTTACCTT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG      1150
   CCGGGCGCGT GACATGCATC GGTGGGCCAA AACCGGAGGG CTCAGTAACC      1200
   ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC      1250
35 GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC      1300
   TTGCGCAACG TAAACACTTT CTTTCTGTTA ATTGGCTCAT TTCCTATTCA      1350
   AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA      1400
   CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT      1450
   TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC      1500
40 AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA      1550
   GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT      1600
   GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA      1650
   GCTGAGTCCG CTGGGGAAC TAAAGATTAC TGGAAC TACA TTCGTGAAAT      1700
   GATTCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC      1750
45 AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA      1800
   ATTGTCAGCG CATTGCCTTC GCTGCTGCAA TAA                      1833

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50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
(B) STRAIN: HB8
(C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCCGGCGG	TGATCGCCAA	50
GGGCATGCTC	GGGGCCCCGA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
GCCTCGTGGG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	CTTCGTCCAG	150
10 GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCCC	CGGGATGCTG	AACGGCATCT	250
ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
GGCCTGGACG	CCCATGGTCA	AGCCCCGGGA	CGAGGTGCGG	GGGGGTATGG	400
15 TCCTGGGCAC	GGTGCCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCCGCCG	GGGAGTACAC	500
CGTGGAGGAG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
ACCAACCTG	GCCCCTTCGC	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGGACG	TCCTCTTCCC	650
20 CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
AGACCGTGAC	CCAGCAGTCC	CTGGCCAAGT	GGTCCAACGC	CGACGTGGTG	750
GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
GGAGTTCCCC	GAGCTCACCG	ACCCCAAGAC	GGGTGGGCCC	TTGATGCACC	850
GCACCGTCC	CATCGCCAAC	ACCTCCAACA	TGCCCCGTGGC	CGCCCCGCGAG	900
25 GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
CTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCCGCCA	GGAGGGCTAC	1050
CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCG	TTCTACGAGC	GGGCGGGCAA	1100
GGTCATCACC	CTGGGCGGCG	AGGAGGGGCG	GTCGACCATC	GTGGGGGCCG	1150
30 TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCCG	1300
CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
CGCGACGCCA	TCTCCGAGCT	TTTGCAGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
35 CGTCCAGCTC	GTGGGGCCCG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
CACGAGGTGG	ACGCCTACTG	CTCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
TTTCCATAGA	CGAGATCCTG	CAGCTCCCCG	TTCTGGAGCG	CATCGGCCGC	1650
40 GCCCGCTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
CCTTCTGA					1758

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTTGTG C

21

60

2) INFORMATION FOR SEQ ID NO: 695

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

15 GTTTCACGTG ATGACGTACA 20

2) INFORMATION FOR SEQ ID NO: 696

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

30 ATIGGICAYR TIGAYCAYGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 697

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

45 CCIACIGTIC KICCRCCYTC RCG 23

50 2) INFORMATION FOR SEQ ID NO: 698

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

5
TGTTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC 50
TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA 100
CCGTACTGGC TAAACCTAC GCGGGTGCTG CTCGTGCATT CGACCAGATC 150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA 200
10 CGTTGAATAC GACACCCCGA CCCGTCCTA CGCACACGTA GACTGCCCCG 250
GGCAGCCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC 300
GGCGCGATCC TGGTAGTTGC TCGCACTGAC GGCCCGATGC CGCAGACTCG 350
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 400
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 450
15 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 500
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 550
AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT 600
CCGGAACCGA AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 650
CGTATTCTCC ATCTCCGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 700
20 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG 750
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 800
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 850
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 900
CCGCACACCA AGTTCGAATC TGAAGGTAC ATTCTGTCCA AAGATGAAGG 950
25 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 1000
GTACTACTGA CGTGA CTGTTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 1050
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 1100
CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG 1150
30 TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA 1185

2) INFORMATION FOR SEQ ID NO: 699

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

45 GTIACIGGYT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 700

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

60

5 2) INFORMATION FOR SEQ ID NO: 701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

20

2) INFORMATION FOR SEQ ID NO: 702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

35

2) INFORMATION FOR SEQ ID NO: 703

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

50

2) INFORMATION FOR SEQ ID NO: 704

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG 20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA 20

25 2) INFORMATION FOR SEQ ID NO: 706

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

TGAAATCTTC ACATCCAACA 20

40

2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTT AGTACCTTCT GGTA 25

55

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 26 bases

401

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATIIAT

26

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 25 (C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
30	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAAGATA	AAAAGTGGA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
	AATTGAGGGA	ACTGTTCCACC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACCTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTTCTTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
45	AATGGACAGG	ACTTGTATTA	TTTGTAAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTCTTAA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	TGGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTAAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGGTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAAATT	CATTTGATTG	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAACT	1500
	AACCTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650
 ATTTAG 1656

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2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: extracted from AE000520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

	GTGATCAAAG	ACGATGTGGT	TACAGGCCGT	GTAAGTGAGGG	TGTCTGGTCC	50
	CATTGTGTAT	GCCGAGGGCC	TCTCTGCGTG	CAGCGTATAC	GATGTTGTCTG	100
25	ACGTAGGGGA	AGCATCGCTC	ATCGGAGAAA	TTATCCGGTT	GGATGAGAGC	150
	AAGGCGGTCTG	TGCAAGTATA	CGAGGATGAC	ACAGGTATGC	GAGTCGGGGA	200
	GAAGGTGACA	AGCTTGCGTC	GACCACTCTC	AGTCCGCTTA	GGGCCTGGAT	250
	TAATCGGCAC	CATTATGAC	GGTATTCAGC	GCCCCTTGA	GCGCCTCTTC	300
	CAAGAAGACG	GCGCCTTCTT	GCGTCTGGT	GCGCGTTCAC	AACCGCTTGA	350
30	TGGCTCCGTA	CGCTGGGATT	TTCGTCTCTCA	TTGTAACGAG	CGCGGTGAGG	400
	CCCTGTGCGC	GGGGATTCCG	ATTGCACCTG	GGTCAGTGTT	AGGGACCGTG	450
	CAGGAGACTC	CTTCTGTTGT	GCACACTATC	ATGGTTCCTC	CTGACATCCG	500
	GGGGAGCGTG	CTATCTTCGT	TCAAGGGCGC	AGGTGCTTAC	ACAATAGATG	550
	AAGAAATTGG	ACGCACTGAT	CTTGGTGAGC	CGCTTTTCT	ATCCCAGTAC	600
35	TGGCCAGTGC	GTCGTGCGCG	TCCTTTCAGC	AAAAAACTTG	CAGTGTGTGA	650
	GCCACTAGTT	ACTGGACAGC	GGGCGATTGA	TGTTTTCTTC	CCCCTATCAA	700
	AGGGAGGAAC	GGCGGCTATT	CCAGGGGGAT	TTGGAACCTG	GAAGACAATG	750
	ACGCAGCATG	CCGTTGCCAA	GTGGTGTGAT	GCAGATATTA	TCGTGTACAT	800
	CGGCTGCGGA	GAGCGGGGCA	ACGAGATGAC	AGACGTGCTC	TCTGAATTTT	850
40	CCAAACTCAT	CGATCCGCGC	ACAGGACGCT	CTCTTATGGA	GCGGACGATT	900
	TTGATCGCAA	ATACGTCCAA	TATGCCTGTG	TCCGCACGCG	AGGTGTCGCT	950
	GTATTCAGGG	ATTACCCTTG	CGGAATACTA	CCGTGATATG	GGTATGCATG	1000
	TGGCCATCAT	GGCTGATTCT	ACCAGCCGCT	GGGCGGAGGC	GCTGCGTGAA	1050
	TTGTCTGGGC	GCATGGAAGA	AATGCCTGCG	GAGGAGGGAT	TCCCTGCGTA	1100
45	CCTTCCGACG	CGTCTTGCAG	AATTTTATGA	GCGCGCAGGA	CGCGTGGA	1150
	CCTGTGTGGC	GCGCGAGGGC	TCTGTGAGCA	TCATTGGTGC	TGTTTCTCCC	1200
	CTGGGTGGAG	ATTTCTCTGA	GCCGGTGACG	CAGCACACAA	AGCGCTTCAT	1250
	CCGTTGCTTT	TGGGCCTTGG	ATCGTGAAC	TGCACACGCG	CGTCATTACC	1300
	CTGCCATTGG	GTGGATAGAT	TCATACTCTG	AATATGCGCA	GGAAGTAAGT	1350
50	GCATGGTGGA	GTAAGTATGA	CCCAGCGGCA	GGCGGTTG	GCGCCGAGC	1400
	CTTGGATTTG	CTGAGAAAGG	AACAGCGGTT	ACAGCAAATT	GTCAGGCTTG	1450
	TCGGTCTCTGA	TGCGCTGCCT	GGAGAAGATC	GTCTGGTGCT	AATGGTGTGT	1500
	GAAATGATCA	AAGGTGGCTT	TCTGCAGCAG	AACGCTTTTG	ATCCGACGGA	1550
	TGTGTTCTCC	TGTCCCGAAA	AGCAGGTGCA	GATCTTGCGT	ACCATAGTGG	1600
55	ATTTTACGA	ACGTGCCGTG	GTGCTGCTGC	GTGCAGGTAT	TTCGCTTTCT	1650
	GCGCTGTCCC	AGCTTTCGTG	CCGGGAGCTC	ATCGTACGTA	TGAAAACCTAC	1700
	GTACGGGAAT	GAGGATGTAC	ACAAGATGCA	GAAAGTGTAC	GACACGATGT	1750
	GCACTGAGTT	TGACCAACTG	AGTGTGTGTG	CTGCCGCGCG	CACACAAGGG	1800
60	GGGGAGAAAG	TCGAATGA				1818

2) INFORMATION FOR SEQ ID NO: 711

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia trachomatis*
 15 (B) STRAIN: MoPn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
20	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTGAAG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACTTTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
25	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTC	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
30	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTAGAA	600
	GGGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
35	TGTAGAAATT	CTTCAGGAGT	TCCCGCATT	GACAGATCCT	CATACGGGGC	850
	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTTCA	GGCGATTAGA	AGAAATCCCT	1050
40	GGAGAAGAAG	CTTTCCAGC	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTA	1100
	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGAGCAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
45	CTAAGTACTT	GGATTCTGTG	GCGGAGATT	TAGAGAAAAA	AGTTCCAGGA	1350
	TGGGGAGATT	CCGTTAAAAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400
	AATTGGTAAG	CGAATAGAAG	TTGTTGGGGA	AGAAGGGATT	TCTATGGAAG	1450
	ATATAGAAAT	CTTTTTGAAA	TCAGAGTTGT	ATGATTCTCT	TTACTTACAG	1500
	CAAAACGCTT	TCGATGCAGA	GGACTGTTAT	TGTCCTTTTG	ATCGTCAAAT	1550
50	AGAGCTTTTT	TCTTTAATGA	GTCATATTTT	TAGCTCTAGA	TTCTGTTTTG	1600
	ATTGTCCAGA	TAATGCTCGG	AGTTTCTTTT	TAGAGCTTCA	AAGTAAAATT	1650
	AAAACGCTGA	ATGGTCAAAA	ATTCTTTTCT	GAAGACTATC	AGAAGGGGCT	1700
	AGAAGTGATC	TATAAACTAT	TAGAAAGCAA	AATGGTGCAG	ACGGCGTAGG	1750
55	TATGCAAACA	ATATATACAA	GAATTACGG			1779

2) INFORMATION FOR SEQ ID NO: 712

- 60 (i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

GTGCAAATTG GAAAAATTGT CAAAGTTTCA GGTCTTTTGA TTTTAGCTGA 50
 15 AAACATGTCA GATGCTAGTA TCCAAGACAT TTGTCATGTA GGAGATTTAG 100
 GCGTTATCGG AGAGATTATT GAAATGCGAG GCGACGTCGC TTCGATTCAA 150
 GTATATGAAG AAACAACAGG CATTGGACCA GGAGAACCAG TTATTTCAAC 200
 AGGAGAACCA TTATCTGTTG AATTAGCCCC AGGTTTAATT GCCGAAATGT 250
 TTGATGGTAT TCAACGACCA TTGGATACAT TTCAAGAAGT AACCCACAGT 300
 20 AACTTTTTAG GCCGTGGCGT TAAAATTGAT GCGTTAGATC GTGAGAAAAA 350
 ATGGACGTTT GAACCAACTG TGGCAGTTGG TGAAGAAGTG TCGGCAGGTG 400
 ACATCGTCGG TGTGGTTCAA GAAACACCGA TTATTCAACA TAAAATTATG 450
 GTGCCTTTTCG GCGTTTCAGG AACGATTGCC GAAATTAAAG CAGGTGACTT 500
 TGCCATTGAT GAAACAGTTT ACTCAGTGGA AACGGCTAAA GGAACGGA 550
 25 GTTTTAGCAT GATGCAAAAA TGGCCCGTTC GGCGGGGACG TCCCATTTTA 600
 GAAAAACTAA GTCCCAAAGT ACCGATGGTG ACCGGACAAC GCGTAATTGA 650
 TACCTTTTTT CCAATTACGA AAGGCGGAGC GGCAGCAGTT CCAGGACCAT 700
 TTGGCGCTGG AAAAACAGTC GTTCAGCACC AAATTGCTAA GTGGGCCGAT 750
 GTCGACTTAG TCGTTTACGT TGGTTGTGGG GAACGCGGGA ATGAAATGAC 800
 30 AGATGTTTTA AATGAATTC CAGAATTAAT TGACCCAACA ACTGGTGAGT 850
 CTTTGATGAA TCGGACGATT TTAATTGCGA ATACGTCAAA TATGCCGGTA 900
 GCGGCACGGG AAGCCTCGAT TTATACAGGG ATTACCATTG CAGAATATTT 950
 CCGTGATATG GGTAA 965

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2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: extracted from J04836

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

GTGGAAGTAA AAGGTGAAAT TTATCGTGTG TCTGGGCCTG TCGTCACCGC 50
 CATCGGCTTG CAGGCAAAAA TGTATGACCT GGTCAAAGTC GGTAATGAAG 100
 55 GTTTAATGGG TGAAGTCATT CAGATATTAG GGCCCAAGAC CATCATCCAG 150
 GTATATGAAG AGACCGCAGG TATCAAGCCA GGGGAACCCT GTGTATCTAC 200
 AGGGTCGTCT CTGTCCGTAG AACTTGGTCC GGGTCTTCTT TCCAGTATTT 250
 ATGACGGGGT TCAAAGGCCCT CTGCACGTCC TGCTTGAAAA AATGGGTAGC 300
 TTCATCCAGA GAGGTGTCAG CGCAGATGGG CTTGATCATA AGAACTCTG 350
 60 GGATTTCAAA CCCATTGTCA AGAAGGGCGA TTCCGTAAAA GGTGGAGACG 400

405

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTTGA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAACCTGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTACTGTTCT	TATCGCTAAC	ACTTCAAAAC	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTT	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTCTTG	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCCTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

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2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
 (C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTACTGGAGC	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAAGTGT	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTTA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAGAG	AACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCG	G TTCAGGAAA	AACGGT TACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTGCT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1354 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: W83

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACCG	GAAAGACCAC	AATGTAACCA	450
	TGGTGACAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAAC TGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	G TAGAGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950

	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTCGGTA	ACGTTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
5	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354

2) INFORMATION FOR SEQ ID NO: 716

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGACTCAA	GGGAAGATTA	TAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
30	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
	GGGTTAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
35	TGATTTTCTA	GTTCGTGGGG	TAGAAGTTCC	AAGTTTGGAT	AGAGATATTA	350
	AGTGGCATT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAAGTGTCAA	GGAAACCGAG	GTAAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
40	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	CTTTCAGTA	ACCAAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
45	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
	CAATCAATTA	TGCAACGGAC	AGTTCTGATT	GCTAATACTT	CAAATATGCC	900
	TGTTGCTGCT	CGTGAGGCTT	CAATTTATAC	AGGAATTACC	ATGGCTGAGT	950
	ATTTTCGTGA	TATGGGCTAC	TCTGTGCGCA	TTATGGCTGA	TTCAACTTCA	1000
	CGTTGGGCAG	AAGCGCTACG	TGAAATGTCA	GGACGTCTAG	AAGAAATGCC	1050
50	TGGTGATGAG	GGTTATCCTG	CTTATCTGGG	AAGTCGTATC	GCTGAATATT	1100
	ATGAAAGAGC	AGGACGTTCT	CAGGTTCTAG	GGCTTCCAGA	ACGTGAAGGA	1150
	ACGATTACTG	CTATTGGAGC	TGTATCGCCA	CCTGGTGGAG	ATATTTTCAGA	1200
	ACCAGTTACT	CAAAACACTT	TACGGATTGT	GAAAGTTTTT	TGGGGGCTTG	1250
	ATGCTCCGTT	GGCACAGCGA	CGTCATTTTC	CTGCAATTAA	CTGGCTTACA	1300
55	TCTTATTAC	TATATAAAGA	CAGTGTGGGC	ACTTATATAG	ATGGTAAAGA	1350
	GAAGACAGAT	TGGAATAGTA	AAATAACTCG	TGCGATGAAC	TACTTACAAC	1400
	GGGAATCTAG	TTTAGAGGAA	ATTGTTTCGTC	TTGTTGGAAT	TGATTCTCTG	1450
	TCTGATAATG	AACGACTAAC	GATGGAAATT	GCTAAACAAA	TTGAGAGAAG	1500
	TTATTTGCAA	CAGAACGCTT	TTGATTCCGT	AGATACATTC	ACTTCGTTTG	1550
60	CAAAACAAGA	AGCAATGCTA	AGTAATATTC	TCACTTTTCG	TGATCAGGCA	1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

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2) INFORMATION FOR SEQ ID NO: 717

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
25 CACATCCTGC	TGGCGCGTCA	GGTCGGTGTTG	CCGTACATCA	TCGTGTTCTT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TCGAAGTACG	ACTTCCCGGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGCGCAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
30 TCCCGACGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCTGAT	GCCGGTGGAA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCGA	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
35 GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCGCC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	GCTGCCGAAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTGATCA	CGGTGAAGCT	GATCGCGCCG	800
40 ATCGCGATGG	AAGAAGGTCT	GCG			823

2) INFORMATION FOR SEQ ID NO: 718

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

60 GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
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	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATGGTGTTC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCAGCGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTT	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

20 2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)
 (B) STRAIN: ATCC 8260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAGAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAACT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

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2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*

(B) STRAIN: ATCC 14501

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

	GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
	TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAACTGAT	CGACCTTGTT	150
15	GAAATGGAAG	TACGTGAGCT	GTTAAGCGAG	TACGGATTCTG	ACGGAGATAA	200
	CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
	AATACGTTGG	CGCTATCAAA	GAACCTGATG	ATGCAGTTGA	TGAATTCATC	300
	CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCCTGATGT	CTGTAGAAGA	350
	CGTTATGACA	ATCACAGGAC	TGGGTACAGT	TGCTACAGGA	CGTGTTGAGC	400
20	GTGGGGTAGT	AAAACCTGGGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
	ACTCAGAAAA	CTGTTGTTAC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
	CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
	GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
	CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
25	TGGACGTCAC	ACTCCATTCT	TTTCTAACTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
	GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

30

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 789 bases
35	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

	TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
	TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
	AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
50	GAGAATTATT	AAGCGAATAC	GGATTGACG	GAGACGAATG	TCCAGTAGTA	200
	GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
	AGACTTAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
	CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
	AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
55	AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
	TCACAGGAGT	AGAAATGTTT	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
	GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
	AGGTCAAGTA	CTAGCAAAAC	CAGGTTTCAGT	AACACCTCAC	AAAAAATTCG	600
	TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
60	TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAC	700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC 750
 ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

5

2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

GTTCAGCAGC AGACGGTCCA ATGCCACAAA CAAGAGAACA TATACTACTA 50
 GCATCAAGAG TTGGTGTTGA CTATATCGTA GTATTCTTAA ACAAGGCAGA 100
 TATGGTAGAT GACGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTAGAG 150
 25 AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATCAAG 200
 GGATCAGCTT TAGTAGCATT AGAAAACCCA ACAGATGAAA AATCAATCGC 250
 TCCAATCTTA GAATTAATGG AAGCAGTAGA TAGCTACATT CCAACACCAG 300
 AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTACAC 350
 ATAAGTGGTA GAGGAACAGT TGCAACAGGA AGAGTTGAAA GAGGAGTTCT 400
 30 TCATGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GAAAGCAGAA 450
 AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCA 500
 CAAGCTGGAG ATAATGTTGG AGTACTTTTA AGAGGTGTTC AAAGAACAGA 550
 TATCGAAAGA GGTCAAGTAT TAGCAAAGAC TGGATCAGTT AAGCCACACA 600
 GCAAGTTCGT AGGTCAAGTA TACGTACTTA AGAAAGAAGA AGGTGGAAGA 650
 35 CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC 700
 AGACGTTACT GGATCAATCA AATTACCAGA CGGAATGGAA ATGGTTATGC 750
 CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCAA 798

40

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

GTTCAGCAGC AGATGGTCCA ATGCCTCAAA CAAGAGAACA CATACTACTA 50
 GCTTCAAGAG TTGGTGTTGA CTACATAGTT GTTTCTTAA ACAAGGCAGA 100
 TATGGTAGAT GACGAAGAAT TATTAGAATT AGTTGAAATG GAAGTAAGAG 150
 60 AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATAAAG 200

	GGTTCAGCTT	TACAAGCATT	AGAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACCTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCCACA	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAACTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
	AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

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2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
 (B) STRAIN: ATCC 19406

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATTA	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

50

2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

413

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*

(B) STRAIN: ATCC 43197

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTC	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCCA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCAGTTCGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTGCAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

2) INFORMATION FOR SEQ ID NO: 726

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus sulfureus*

(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACCTCGT	ACACTGACAA	ACCATTTCAT	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GATAGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GGCGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*
(B) STRAIN: ATCC 49156

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACC	TATTGTCTGA	150
15	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
20	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
25	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma pirum*
(B) STRAIN: ATCC 25960D

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

	GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCTTAAAA	TGGTTGTTTT	100
45	CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
	CTGAAGAAGT	AAAAGACTTA	TTAAAATCTT	ATGGTTTTGA	TGGTGACAAT	200
	ACTCCAATTA	TCGTGGTTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
	ATGAGAAGAA	AAAATTAAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
	CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
50	GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
	TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
	CATTTAAATC	TGTTGTAAAC	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
	GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
	TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
55	CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
	GGTCGTCATA	CTGCTTTCTT	AAACGGTTAT	CGTCCTCAAT	TCTATTTTCA	700
	AACAACCTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
	TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
60	GCTTGTAATA	AGGAAGTAAG	TTT			823

2) INFORMATION FOR SEQ ID NO: 729

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycoplasma salivarium*
 15 (B) STRAIN: ATCC 23064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

	GGAGCAATCT	TAGTTGTTGC	TGCAACTGAT	GGTGCGATGC	CTCAAACCTCG	50
20	TGAACACGTT	TTACTTGCAA	AACAAGTTGG	TGTTCTCTAAA	ATCGTTGTTT	100
	TCTTAAACAA	AATCGATATG	TTCAAGCCAG	AAGAAAGAGC	CGAAATGGTT	150
	GAAATGGTTG	AAATGGACAT	TCGTGACTTA	TAAACAAAT	ACGACTTTGA	200
	TGGTGACAAT	ACTCCTATTA	TTGCTGGTTC	AGCATTAAAA	GCATTACAAG	250
	GTGATCCAGA	ATATGAAAAG	AATATTCTAG	AACTTATGGA	TGCAGTAGAC	300
25	ACATACATTG	ATGAACCTAC	TCGTGATAAA	GATAAACCAT	TCTTAATGGC	350
	TGTAGAAGAC	GTATTTACAA	TTACTGGTCG	TGGAAGTGTT	GCTACTGGTA	400
	GAGTAGAACG	TGGTACATTA	CATCTAAATG	ATGAAGTTGA	AATCGTTGGT	450
	CTACGTCCAA	CAATTAAAAAC	TGTTGTTACT	GGAATTGAAA	TGTTCCGTAA	500
	AAATTTAAAA	GAAGCTCAAG	CTGGAGATAA	TGCAGGACTT	TTACTACGTG	550
30	GAATTGATAG	AGATCAAGTA	GAACGTGGAC	AAGTTTTGGC	CAAACCAAAA	600
	AGTATTATTC	CTCACACAGA	ATTTGAAGCT	GCTGTGTATG	TTCTAAAAGC	650
	TGAAGAAGGT	GGACGTCACA	CTCCATTCTT	TGAACACTAT	AAACCACAAT	700
	TTTACTTTTCG	TACAACCGAC	GTTACTGGTG	GAATTAAATT	CAAACCTGGA	750
	CGTGAAATGG	TTATGCCTGG	CGAAAATGTT	GAATTTACAG	TTACTTTAAT	800
35	TGCTCCTATT	GCAGTTGAAG	AAGGAA			826

2) INFORMATION FOR SEQ ID NO: 730

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

55	TGGTATGTTT	CGCAGCYGAY	GGYCCTATGC	CTCAAACCTCG	CGAACACATC	50
	CTGYTGGCTC	GCCAAGTAGG	YGTACCTTAC	ATCATCGTRT	TCATGAACAA	100
	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	GAAATGGAAA	150
	TCCGYGACCT	GYTGTCMAGC	TACGACTTCC	CMGGCGACGA	CTGCCCAATC	200
	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGYGAYGCTG	GTTACGAAGA	250
60	GAAAATCTTC	GAAYTGGCTG	CTGCTTTGGA	CAGCTACATC	CCAACTCCTG	300

	AGCGTGCTGT	GGACAAACCK	TTCYTGYTGC	CTATCGAAGA	CGTRTCTCT	350
	ATCTCTGGYC	GYGGTACMGT	AGTAACYGGY	CGTGTAAGAC	GCGGTRTCAT	400
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450
	CCACTTGTA	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCGT	GGTACCAARC	GTGAAGACGT	550
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600
	AATTCAAAGC	AGAAGTATAC	GTAAGTACCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCTAATA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800
	AAGGTCTGCG					810

15 2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
35	GTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GAATCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
45	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
	CGACGGTCTG	CGT				813

50

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

417

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
5 (B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

```

10 CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT      50
   CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG TTCCTGAACA      100
   AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT TGAAATGGAA      150
   GTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT      200
   CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG      250
   CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA      300
15 GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC      350
   CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA      400
   TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG      450
   TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTGTTG ACGAAGGCCG      500
   TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA CGTGAAGAAA      550
20 TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC      600
   AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA      650
   CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG      700
   ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG      750
   GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA TCGCAATGGA      800
25 CGACGGTCTG CG                                812

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2) INFORMATION FOR SEQ ID NO: 733

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

```

45 TGGTTGTTGC TGCGACTGAC GGYCCGATGC CGCAGACCCG TGAGCACATC      50
   CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA      100
   ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG      150
   TTCGYGAAC TGTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC      200
50 GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC      250
   GAAAATCATC GAAGTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG      300
   AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC      350
   ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC GCGGTATCAT      400
   CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT      450
55 CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT      500
   GCGGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT      550
   CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA      600
   AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG CCGCCGTCAT      650
   ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA      700
60 CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG      750

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CGGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 800
GACGGTCTGC GTTT 814

5

2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Virchow
(B) STRAIN: ATCC 51955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAATGGCTG GCTTCCTGGA TTCTTACATT 300
CCGGAACCAAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCGGT CGTGTAGAAC 400
GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
35 CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG 650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCAATGGAC GACGGTCTGC GTTTCGCA 828

40

2) INFORMATION FOR SEQ ID NO: 735

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
55 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG 50
60 TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAACCTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAAGAC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTGCACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCTCTA	TTCACCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
	CTCCAGAGAG	AGATACAGAT	AAACCATCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
45	CAAGCACAAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAAT	TCTATTTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

420

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

10	GTCAACATGA	TGGAGCTCAT	CAACAACATC	GCGAAGGAGC	ACGGCGGTTA	50
	CTCCGTGTTT	GCGGGCGTGG	GCGAGCGTAC	CCGTGAAGGG	AACGACTTCT	100
	ACCACGAAAT	GAAGGACTCG	AACGTTCTCG	ACAAGGTCGC	GCTGGTGTAC	150
	GGCCAGATGA	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTGG	CGCTGACGGG	200
	CCTCACGATG	GCCGAGCACT	TCCGTGACGA	AGGCCTCGAC	GTGCTGTTCT	250
15	TCGTCGACAA	CATCTACCGT	TTCACGCTGG	CCGGTACCGA	AGTGTCGGCG	300
	CTGCTCGGCC	GTATGCCGTC	GGCAGTGGGC	TATCAGCCGA	CGCTGGCTGA	350
	AGAAATGGGC	AAGCTGCAAG	AGCGCATCAC	GTCGACGAAG	AAGGGCTCGA	400
	TCACGTCGGT	T				411

20

2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
35 (B) STRAIN: ATCC 638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

	TACAAGAGCT	TATTAACAAT	ATAGCTACTC	AACACGGTGG	TATATCAGTA	50
	TTCGCAGGTG	TTGGAGAGAG	AACAAGAGAA	GGTAACGACT	TATTCCATGA	100
40	GATGAGCGAT	ACAGGAGTTA	TAAATAAAAC	AGCTCTAGTA	TTCGGACAAA	150
	TGAATGAGCC	ACCTGGAGCA	AGAATGAGAG	TTGCTTTAAC	TGGTCTTACA	200
	ATGGCTGAAT	ACTTCAGAGA	TCAACAAGGG	CAAGACGTTT	TATTATTCGT	250
	AGATAATATA	TTCCGTTTCA	CTCAAGCAGG	ATCTGAGGTT	TCTGCACTTC	300
	TTGGACGTAC	TCCATCAGCA	GTTGGATACC	AACCAACATT	AGCAACAGAG	350
45	ATGGGTAGAT	TACAAGAGAG	AATAACATCT	ACAAATAAAG	GGTC	394

2) INFORMATION FOR SEQ ID NO: 739

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)
 (B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

	TTAATAAACA	ACATAGCTAA	ACAACATGGT	GGTTTATCAG	TATTTACTGG	50
	AGTTGGTGAA	AGATCAAGAG	AAGGTAATGA	CTTATATCAT	GAAATGAGAG	100
	AGTCAGGAGT	TATTGATAAG	ACAGCATTAG	TATTTGGACA	AATGAATGAG	150
10	CCACCGGGTG	CCAGAATGAG	AGTTGCATTA	ACAGGTCTTA	CTATGGCAGA	200
	GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
	TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
	CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
15	TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

	TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
35	GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
	GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
	CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
	CATTTTAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
	ATTCGGTTTC	ACACAAGCTG	GTTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
40	TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium ramosum*
- (B) STRAIN: ATCC 25582

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

60

	TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
	AGTTTTTGCT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
	ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
	CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
5	TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
	TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
	TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
	CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

10

2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12964

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
30	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAACATA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTGG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
35	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

2) INFORMATION FOR SEQ ID NO: 743

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTAGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
60	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

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2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

TTCCCCCGCA CGCATGCCCA AGGTGTTCTGA TGCCCTGAAG CTCGACGGCT 50
CGGCCCTGAC GCTGGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
ACCATCGCCC TGGGTTTCGTC CGACGGTCTG CGTCGCGGCC TGATGGTGTG 150
25 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
GTCGCCTTCG CAGGAAGTGC TGGAAACCGG CATCAAGGTG ATCGACCTGA 350
TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTTCG TGGCGCCGGT 400
30 GTGGGCAAGA CCGTGAACAT GATGGAAGTC ATCAACAACA TCGCCAAGGG 450
CCACGGTGGT CTGTGCGTGT TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
GCAATGACTT CTATCACGAA ATGTCGGACG CCGGCGTGGT CAACCAGGAG 550
TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
CCCGGGCAAC CGTCTGCGCG TGGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
35 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCTG 800
AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

40

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
55 (B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

GCCGTACCAC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
60 TCTGGTGCTG GAAGTTCAGC AGCAGCTGGG CGGCGGTATC GTACGTACCA 100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTCGGCGGT	GCGGGTGTAG	400
	GTAAAACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria canis*
 (B) STRAIN: ATCC 14687

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCG	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGGCG	GTAAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
	TAAGTGGCTT	GTCTATGGCC	GAATTCCTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

425

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAGCCG TGCCATTAC CAACTGCTC CGAAATTCGA CGAGTTGTCT 300
 TCAGTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGCGGTA AAGTAGGCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGACTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30

2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTTCGT TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAATCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTGCGTGG TGCAGGTGTG 400
 55 GGTAAGACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTTC TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAGTAGC GATGGTTTAT GGTCAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTG CATTGACAGG CTTGACGATG GCAGAAATAT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGCGGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGT [^] CAGC	750'
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTCG	850
ATCACTTCGG	GG				862

5

2) INFORMATION FOR SEQ ID NO: 749

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

GGA	ACT	CCCA	CGT	GAC	GCTA	TCCC	GCAT	GT	TTTT	GAT	GCA	TTAA	AATT	AG	50
25	TTG	AAA	ATGA	CCT	AACCTTA	GAAG	TTCA	AC	AACT	TTT	TGGG	GGAT	GGT	GT	100
	GTG	CGT	ACCA	TTG	CGAT	TGGG	TAG	TTCA	GAT	GGAT	TAA	AAGC	GTG	GTAT	150
	TGT	GAA	TAA	T	ACCG	GAG	CTC	CGAT	TACT	GT	TCCT	GTT	TGGC	CGT	200
	TGG	GTC	GTAT	CAT	TGG	ATGTA	TTGGG	TAATC	CGGT	TGAT	G	GGCAGG	TCCG		250
	GTAA	ATGC	AT	CCA	ATAC	ACG	TGCG	ATCCAT	CAAG	AGG	CTC	CTAAG	TTTGA		300
30	TGAG	CTTT	TCT	TCA	ACA	ACGG	AATT	ATTAGA	AACT	TGG	CATT	AAGG	TATCG		350
	ACT	TGTT	ATG	TCC	GT	TTGCC	AAAG	GTGGTA	AAG	TAG	GTCT	GTTT	TGGT	GGT	400
	GCG	GGT	GTAG	GTAA	AAC	CGT	AAAT	ATGATG	GAG	TAA	TTA	ACA	ACAT	TGC	450
	CAAG	GCAC	AT	AGC	GGT	TTGT	CTGT	GTTTGC	AGG	CGT	GGGT	GAAC	GTACTC		500
	GTGA	AGGT	A	TGAC	TTCT	TAT	CAC	GAGATGA	AAG	ATT	CCAA	CGT	ATTGG	AC	550
35	AAAG	TGG	CAA	TGG	TTT	ACGG	TCAG	ATGAAC	GAAC	CTCC	AG	GCAAC	CGTCT		600
	GCG	CGT	TGCT	TTG	ACCG	GT	TGAC	TATGGC	CGA	ATACT	TC	CGT	GAC	GAAA	650
	AAG	ACG	AAAA	CGG	TAA	AGGT	CGC	GACGTAT	TGTT	CTTC	CGT	GGAC	AACATT		700
	TAC	CGT	TACA	CTTT	TGG	CCGG	TAC	GGAAGTA	TCC	GCATT	GC	TGGG	TCGTAT		750
	GCCT	TCAG	CA	GTA	GGT	TACC	AACC	GACATT	GGCT	GAA	GAA	ATGGG	TCGTT		800
40	TGCA	AGAG	CG	TATT	ACCT	CT	ACCC	GACAG	GCT	CTATT	AC	TTCC			844

2) INFORMATION FOR SEQ ID NO: 750

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CGCG	ACGCTA	TTCC	GCATGT	TTAC	GATGCC	CTGA	AATTGG	ACG	AGAACGG	50
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	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATAACG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCGC	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neisseria gonorrhoeae*
- (B) STRAIN: ATCC 31426

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

35	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTTCG	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAAGTA	CTGTTGACGA	GGCAGGTCCA	ATTGATAACG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCCGGCGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCAAACCG	GTTCCATTAC	TTCC		834

55 2) INFORMATION FOR SEQ ID NO: 752

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
- 60 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCCG	CATGACTGTG	AGCAATACTG	150
15	GTTCGCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTT	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGTTTGTAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTT	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTC	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCTGGAA	GTCCAACAGC	TTTTGGGTGA	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTAG	TTCAGACGGC	CTGAAACGCC	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTGACGCA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GGCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGCAGG	CGTGGGCGAG	CGTACCCCGC	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

5

2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
25 CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GA CTGTGAGC	150
AATACCGGTG	CGCCCATTAC	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
CATTGTGCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
30 TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGC	GGTGCCGGTG	400
TGGGTAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCCGCGAAGG	500
TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GATAAAGTGG	550
35 CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	ATCTACCGTT	700
ACACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
GCA GTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
40 GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

2) INFORMATION FOR SEQ ID NO: 755

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

60 CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
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430

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTA GTTCGTA	200
	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTTCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGTTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTCGACGCT	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAAGTCTC	CGAAATTCGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

	CCCGTGATGC	TATTCCTCATG	TATACGATGC	CCTGAAATTG	GTAGATAACG	50
	ATCTGACCCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
	ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15	TACCGGCGCT	CCGATTACTG	TTCCGGTGGG	GAAAGCCACC	TTGGGACGTA	200
	TTATGGATGT	GTTGGGTAAT	CCGGTTGATG	AAGCAGGTCC	TGTTGTATCA	250
	GAAGAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
	TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
	GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20	GGTAAACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
	TAGTGGTTTG	TCTGTATTTC	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
	ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
	ATGGTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
	TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25	ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
	ACTCTGGCCG	GTAAGTGAAGT	GTCTGCACTG	TAGGTCGTA	TGCCGTCTGC	750
	AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
	GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

30

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

	CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
	TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
	ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
	TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
	AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
	TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55	TCCGTTTGCA	AAAGGCGGTA	AAGTAGGTCT	GTTCCGGCGT	GCCGGTGTGG	400
	GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
	AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
	TGGTGTACGG	TCAGATGAAT	GAGCCGCCGG	GCAACCGCTT	GCGCGTGGCT	600
60	TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAA	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

5

2) INFORMATION FOR SEQ ID NO: 759

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
- (B) STRAIN: ATCC 33519

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGCT	AAAGGTGGTA	AAGTAGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
GTAAAACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCTTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTAA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
40 AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Enteritidis
- (B) STRAIN: ATCC 13076

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTGCACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTA AAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

20

2) INFORMATION FOR SEQ ID NO: 761

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Yersinia pestis*
- (B) STRAIN: KIM D27

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAACTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAAGT	ATCCTTGGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCAATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCTTC	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCCG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTTCG	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCCCGCGA	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium sordellii*
- (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40

	GAACTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTCGC	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTCGG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 405 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

435

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTG	ACTCAAGCAG	GTTTCAGAGG	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium botulinum*

(B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAAGT	TTCAGCATT	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

45

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium histolyticum*

(B) STRAIN: ATCC 19401

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
5	GAAAGATTCT	GGGGTTATAG	AGAAACTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
- (B) STRAIN: ATCC 9321

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTTCGTC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
- (B) STRAIN: ATCC 46775

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCCTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCG	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTGC	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTCCGG	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCCTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1343 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
- (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTCGTA	TCATGAACGT	CACTGGTGAC	CCCATTGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTACG	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CCTCTTACGC	TGCTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTG	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCAC	GGTGGTTTCT	CTGTCTTCAC	TGGTGTCCGG	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTGAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCACTGTGT	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGTA	GAACCTGCCTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTCGT	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTGTA	CTGACCCCTG	900
	CCCCGCCACC	ACCTTCGCCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCCG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCCG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTCCG	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT CAAGGCTATC TTGACTGGTG AGGGTGACGA CCTTCCCGAG 1300
GGTGAGTCTC GACTATCTCC GCATTCATAG CGTATAACTG ACA 1343

5

2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT GATTGTATGT TCACCTGCAA CATAAGACTT CCCATTCTCC 50
ACTCTTTTCT AACTCTTCAC AGAACAACAT TGCCAAGGCT CACGGTGGTT 100
ACTCTGTCTT CACTGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGATCTG 150
25 TACCACGAAA TGCAGGAGAC TGGTGTCAAT CAGCTCGAGG GTGAATCTAA 200
GGTCGCCCTT GTCTTCGGTC AGATGAACGA GCCCCAGGT GCCCGTGCCC 250
GTGTGCCCTT TACCGGTCTG ACCATCGCCG AGTACTTCCG TGACGAGGAA 300
GGTCAGGATG TGCTGCTCTT CATTGACAAC ATTTTCCGTT TCACCCAGGC 350
CGGTTCTGAG GTGTCTGCC TTCTTGGTGC TATCCCCTCC GCTGTCGGTT 400
30 ACCAGCCAC TCTGGCCGTC GACATGGGTG GTATGCAGGA GCGTATTACC 450
ACCACCACCA AGGTTTCCAT TACCTCCGTC 480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

CTCGAACAAG AYAACCTGCC YGCCATTTTG AACGCCCTTG AAGTCAAGGA 50
YCACTCTGGT GGACGTCTCG TYCTCGAAGT CTCTCAACAT TTGGGTGAGA 100
ACACTGTCCG TACTATTGCT ATGGATGGTA CTGAAGGTAA GTTATGTYCA 150
TCCCANNGGA TACAGTCARA CAGMAATGTC TAGTGGTTAT AGCAGYAGCA 200
55 GATGATTGAC CAATATGTTA GGTCTTGTCC GGTGGTCAAA AGGTTGTTGA 250
CACTGGTGCT CCCATTACCA TCCCCGTTGG TAAGGAAGTC CTTGGTCGTA 300
TCATCAACGT TATTGGTGAA CCCATTGATG AACGTGGTCC CATTGACGCC 350
AAGACTCACC GTCCTATTCA CGCTGAAGCT CCCGAATTCG TTGATCAATC 400
CCCCACTCCC GAAATCCTCG AGACTGGTAT CAAGGTYGTC GATTTGTTGG 450
60 CTCCTTATGC TCGTGGTGGT AAGATTGGTC TCTTCGGTGG TGCTGGTGTG 500

	GGTAAGACTG	TCTTGATTCA	AGAATTGATT	AACAACATYG	CCAAGGCTCA	550
	CGGTGGTTAC	TCTATCTTCT	GTGGTGTCTCG	TGAACGTACT	CGTGAGGGTA	600
	ACGATTTGTA	CCATGAAATG	ATTGAAACCG	GTGTCATTCA	ATTGGAAGGC	650
	GAGTCCAAGT	GTGCTCTCGT	CTTTGGTCAA	ATGAACGAAC	CCCCAGGTGC	700
5	TCGTGCCCCG	GTCGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCCGTG	750
	ATGATGAGGG	TCAAGATGTC	TTGCTTTTCA	TTGATAACAT	TTTCAGATTC	800
	ACTCAAGCTG	GTTCTGAGGT	ATCTGCCCTT	TTGGGTCTGA	TTCTTCCGC	850
	TGTCGGTTAC	CAACCCACTC	TTTCCACYGA	TATGGGTGGT	ATGCAAGAGC	900
	GTATTACTAC	CACCAAGAAC	GGTTCCATTA	CCTCCGTCCA	AGCTGTCTAC	950
10	GTCCCTGCTG	ATGATTTGAC	CGATCCTGCT	CCTGCCACCA	CTTTTGCTCA	1000
	CTTGATGCC	ACCACTGTCT	TGTCTCGTTC	CATCGCTGAA	TTGGGTATCT	1050
	AYCCCCTGT	CGATCCTCTT	GATTCCAAGT	CTCGTATCCT	CGATCCCCGT	1100
	ATTGTCGGTG	ATGAGCACTA	CAAGGTTGCC	ACTGAAGTTC	AACAAATCCT	1150
	CCAAAACACTAC	AAGTCTCTCC	AAGA			1174
15						

2) INFORMATION FOR SEQ ID NO: 772

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
- (B) STRAIN: ATCC 24292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

	AGGAGCTTAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
35	ACTGGTGTCTG	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	100
	GCAAGAGACT	TCCGTCATTC	AGCTTGACSG	CGAGTCCAAG	GTCGCTCTCG	150
	TGTTCCGGTCA	GATGAACGAG	CCCCCGGGTG	CCCGTGCCCCG	TGTTGCCCTG	200
	ACTGGTCTTA	CCATCGCTGA	GTACTTCCGT	GATGCCGAGG	GTCAGGATGG	250
	TAAGTTCTAT	AACCTTTGTC	GCAAAGGTTT	CATTCTGGTC	GCTAACTTGC	300
40	TCAGTGCTCC	TGTTTCATCGA	CAACATTTTC	CGTTTCACCC	AGGCTGGTAT	350
	GGAGGTGTCT	GCCCTCCTCG	GTCGTATTCC	TTCTGCCGTC	GGTTACCAAC	400
	CTACTCTCGC	CGTCGACATG	GGTGGTATGC	AAGAGCGTAT	TACCACTACC	450
	AAGAAGGGAT	CCATTAC				467

45

2) INFORMATION FOR SEQ ID NO: 773

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
- (B) STRAIN: ATCC 44331

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

```

15      TTGCCAAGGC CCACGGTGGT TACTCTGTCT TCACTGGTGT CCGTGAGCGT      50
      ACCCGTGAGG GTAACGATCT GTACCACGAA ATGCAGGAAA CCTCCGTCAT      100
5      TCAGCTTGAT GGCGAGTCCA AGGTCGCGCT TGTCTTCGGT CAGATGAACG      150
      AGCCCCCTGG TGCCCGTGCT CGTGTGCTC TTA CTGGTCT TACCGTTGCC      200
      GAGTACTTCC GTGATGAGGA GGGTCAGGAT GGTAAGTTAT ATCGTTTTTA      250
      TTATCTTCTT TGCCACCACC CCTCTACGAA TCCATGCCTC CGTTGGTGAA      300
      GGCATCGTTT GTAGGGCGGG TCGGAGTTTG CGGCAATTTC TGCCGTCGGC      350
10     TTGAAGCCGC GGATGCCCGA TGTTTGACGC GTATCGATGC TAACAACAAT      400
      GACAACAGTG CTTCTCTTCA TTGACAACAT TTTCCGATTC ACCCAGGCCG      450
      GTTCCGAGGT GTCTGCCCTT CTCGGTCGTA TTCCCTCTGC CGTCGGTTAC      500
      CAGCCCACTC TTGCCGTAGA CATGGGTGCC ATGCAGGAAC GTATTACCAC      550
      CACCAAGAAG GGTTCGATTA CCTCCGTC      578
15

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2) INFORMATION FOR SEQ ID NO: 774

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20     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1123 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear
25
        (ii) MOLECULE TYPE: Genomic DNA
        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Rhizopus oryzae
30            (B) STRAIN: ATCC 56015

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

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35     AACTTACCYG CTATCTTGAA CGCTCTCGAA GTCCAAGATC ACTCTGGTGG      50
      ACGTCTTGTC CTTGAAGTTC GCTCAACACT TGGGTGAAAA TACTGTCCGT      100
      ACTATTGCTA TGGATGGTAC TGAAGGTAAG CTATACTATA ACCGKTAT      150
      CCGAGTATGA TATTAAGTTG AAAAAAGGTC TCGTYCGTGG TCAAAGGTT      200
      ATTGACACTG GTGCTCCCAT TACCATTCCCT GYTGGTAAGG AAGTTCTCGG      250
      TCGTATCATT AACGTCATTG GTGAACCCAT CGATGAACGT GGTCCATATCA      300
40     ACGCCAAGAG CCAACGTCCC ATTCACGCCG AAGCTCCCGA ATTCGTTGAC      350
      CAATCTCCTA CTCCCGAAAT TCTTGAAACT GGTATCAAGG TTGTCGACTT      400
      GTTGGCTCCT TATGCTCGTG GTGGTAAGAT TGGTCTTTTC GGTGGTGCTG      450
      GTGTCGGTAA GACTGTGTTG ATTCAAGAAT TGATTAACAA CATCGCCAAG      500
      GCTCACGGTG GTTACTCTAT TTTCTGTGGT GTCGGTGAAC GTACTCGTGA      550
45     AGGTAACGAT CTTTACCACG AAATGATTGA AACTGGTGTC ATCAAGCTCG      600
      ATGGTGACTC CAAGTGTGCT CTTGTCTTTG GTCAAATGAA CGAACCCCA      650
      GGAGCTCGTG CCCGTGTTGC CTTGACTGGT TTGACCATTG CTGAATACTT      700
      CCGTGATGAT GAAGGTCAAG ATGTGTTGCT TTTCATTGAT AACATTTTCC      750
      GTTTCACCCA AGCTGGTTCW GAAGTATCTG CCCTTTTGGG TCGTATTCCC      800
50     TCCGCTGTCTG GTTACCAACC CACTCTTCT ACTGATATGG GTGGTATGCA      850
      AGAACGTATT ACAACCACCA AGAACGGTTC CATTACATCC GTCCAAGCTG      900
      TCTACGTCCC TGCTGATGAT TTGACCGATC CTGCTCCCGC CACCACTTTT      950
      GCTCACTTGG ATGCCACCAC TGTCTTGTCT CGTTCCATTG CCGAATTGGG      1000
      TATTTACCTT GCCGTCGATC CTCTTGAYTC CAAGTCTCGT ATCTTGATC      1050
55     CTCGTATCGT TGGTGACGAA CACTACAAGG TCGTACCGA AGTTCAACAA      1100
      ATCCTTCAAA ACTACAAGTC TCT      1123

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60 2) INFORMATION FOR SEQ ID NO: 775

441

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

15	ATTCAGGAGC	TCATCAACAA	CATTGCCAAG	GCTCACGGTG	GTTACTCTGT	50
	GTTCACTGGT	GTCGGTGAGC	GTACCCGTGA	GGGTAACGAT	CTGTACCACG	100
	AAATGCAGGA	GACTTCGGTC	ATTGAGCTCG	AGGGCGAGTC	CAAGGTCGCG	150
	CTTGTGTTTCG	GTCAGATGAA	CGAGCCCCC	GGTGCCCGTG	CCCGTGTCGC	200
20	CCTTACCGGT	CTGACCGTTG	CCGAGTACTT	CCGTGACGAG	GAGGGCCAGG	250
	ATGGTGAGTA	ACCGACGAAG	TCTGAGATCT	TGTCGGGCAT	TATTCTAACG	300
	ACAAC TAGTG	CTTCTCTTCA	TCGACAACAT	TTTCCGCTTC	ACCCAGGCCG	350
	GTTCCGAGGT	GTCCGCGCTT	CTCGGCCGTA	TCCCCTCTGC	CGTCGGTTAC	400
	CAGCCACCC	TGGCCGTCGA	CATGGGAGGT	ATGCAGGAGC	GTATTACCAC	450
25	GACTCAGAAG	GGCTCGATTA	CCTCGGT			477

2) INFORMATION FOR SEQ ID NO: 776

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

45	TCCGGAGTTG	ATTGTAAGTC	ATTTGAAACC	CAGCCCCAAG	AAACAGAAGC	50
	TAGGCGAAAA	TTGGACAATT	GAGCAATTTA	GCCATTGGAG	AAAAGAAATT	100
	TCGAGTATTA	ATTGTTTTTA	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	150
	TACTCTGTCT	TCACTGGTGT	CGGAGAGCGT	ACCCGTGAAG	GAAACGATCT	200
	CTACCATGAA	ATGCAGGAGA	CCCGTGTCAT	TCAGCTTGAT	GGCGAGTCCA	250
50	AGGTCGCCCT	GGTCTTCGGC	CAGATGAACG	AGCCCCCAGG	TGCCCCGTGCC	300
	CGTGTTGCTC	TTACTGGTTT	GACCATTGCT	GAGTACTTCC	GTGATGAGGA	350
	AGGTCAAGAC	GGTGAGTTTY	TTATGGATAA	AARATTTTTT	TTTTTTTTTT	400
	TTTTTTMAAR	AAATTCATGT	TCTAACAAAG	TATATCCTAG	TGCTTCTCTT	450
	CATCGACAAC	ATTTTCCGTT	TCACTCAGGC	TGGTTCCGAA	GTGTCTGCCC	500
55	TGCTTGGTCG	TATCCCATCT	GCCGTCGGTT	ACCAACCCAC	TCTTGCCGTC	550
	GACATGGGTG	GTATGCAGGA	ACGTATTACC	ACCACCAAGA	AGGGATCCAT	600
	TACCTCCGTC					610

2) INFORMATION FOR SEQ ID NO: 777

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

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GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG      50
GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTCG      100
AGTATTAATT ATTTTATAG AACAAACATT CCAAGGCTCA CGGTGGTTAC      150
20 TCTGTCTTCA CTGGTGTCTGG AGAGCGTACC CGTGAAGGAA ACGATCTCTA      200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG      250
TCGCCCTGGT CTTCGGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT      300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG      350
TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTTT TTCAAGAAAT      400
25 TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT      450
TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC      500
CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT      550
GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC              593

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30

2) INFORMATION FOR SEQ ID NO: 778

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

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CCGTGGTCAA GAAGTTATTG ACACTGGTGC CCCAATTACC ATTCCTGTTG      50
GTCGTGGTAC TCTTGGTAGA ATTATCAACG TCATTGGTGA ACCAATTGAC      100
50 GAACGTGGCC CTATCAAGGC TTCTAAGTAT GCTCCTATCC ATACTGAACC      150
ACCAACCTTT GCTGAACAAT CTACTTCTGC TGAAGTTCTT GAAACCGGTA      200
TCAAGGTTGT CGATCTTCTT GCTCCTTACG CCCGTGGTGG TAAGATTGGT      250
CTTTTCGGTG GTGCTGGTGT CGGTAAGACT GTCTTCATTC AAGAAGTTAT      300
TAACAACATT GCCAAGGCTC ACGGTGGTTT CTCTGTCTTC ACTGGTGTCG      350
55 GTGAAAGAAC CCGTGAAGGT AACGATCTTT ACCGTGAAAT GAAGGAAACT      400
GGTGTCAATCA ACCTCGAAGG TGACTCCAAG GTCGCTCTCG TTTTCGGTCA      450
AATGAACGAA CCTCCAGGTG CCCGTGCCCCG TGTCGCTTTG ACTGGTCTTA      500
CCATTGCCGA ATAATTCCGT GATGAAGAAG GACAAGATGT CTTGCTTTTC      550
GTTGACAACA TTTTCAGATT CACCCAAGCC GGTTCCTGAAG TCTCTGCTCT      600
60 TTTGGGTCGT ATTCCATCTG CCGTCGGTTA CCAACCTACC CTTGCTACCG      650

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	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700
	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTGTA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTT	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Cladophialophora carrionii*
- (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCCAAGTAC	TTCGTACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTGCCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCG	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCTC	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCGT	600
	CGGTCTGTGT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTT	GTCGTGGAAA	CGTTGCTGGT	GACTIONAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCCAGGT	CATCGTCCTC	850
	AACCACCCTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCCA	ATTGCCTGCA	AGTTCTCTGA	GTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

10 TACTTGTA AAA TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT 50
 CTCCTTCAT CAAGAAGATT GGTTACAATC CTAAATCCGT TCCTTTCGTY 100
 CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT 150
 GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG 200
 15 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT 250
 TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG 300
 TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG 350
 GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC 400
 GTTGAAATGC ATCACGAACA ATTGAACAA GGTGTTCCCTG GTGACAACGT 450
 20 TGGTTTCAAC GTCAAGAACG TTTCCGTTAA GGATATCCGT CGTGGTAAACG 500
 TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC 550
 GCTCAAGTTA TCGTCTTGAA CCACCCTGGT CAAATTGGTG CTGGTTATGC 600
 CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT 650
 TATTAGAAAA GATCGATCGT CGTTCCGGTA AGAACTCGA AGATGCTCCT 700
 25 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA 750
 GC 752

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

45 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC T 50
 TCATCAAGAA GGTCGGCTAC AACCCTCAAGC ACGTTCCCTT CGTCCCCATC 100
 TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCTG 150
 GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC 200
 50 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG 250
 CCCCTCCGCC TTCCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC 300
 GGTCCCCGTC GGTCGTGTCG AGACCGGTAT CATCAAGCCC GGTATGGTCG 350
 TCACCTTCGC CCCCGCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG 400
 CACCACGAGC AGCTTACTGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA 450
 55 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGTAAC GTTGCCGGTG 500
 ACTCCAAGAA CGACCCCCC AAGGGTTGCG AGTCCTTCAA CGCCCAGGTC 550
 ATCGTCTCTA ACCACCCTGG TCAGGTCCGT GCCGGTTACG CCCAGTCCT 600
 TGACTGCCAC ACTGCCCACA TTGCCTGCAA GTTCTCCGAG CTCCTCGAGA 650
 AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC 700
 60 AAGTCCGGTG ACGCCGCCAT CGTCAAGA 728

2) INFORMATION FOR SEQ ID NO: 782

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

20	TGAAGTCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
	CGCTAACCTA	TTCACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
25	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
30	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
35	ACGAGCAGCT	TCCCGAGGGT	CTCCCCGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGCAACGTCG	CCGGTGACTC	850
	CAAGAACGAC	CCCCCAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTGCGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
40	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
	GAGGCCTTCA	CCGACTACCC	CCCTCTTGGA	CGTTTCGCCG	TCCGT	1145

45

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

60

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	ATGGTCAACG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATTT	ATAGTTGCGA	CAAGTAACTA	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATTG	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTCGTCCCA	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAAGTCCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTGAAATGTC	750
	ACCACCAGCA	GCTCGTTCAG	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
20	TCGTCTCTAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Mucor circinelloides*
- (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCTT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAACTCATT	650
	GAGAAGATTG	ATCGTCGTTT	CGGTAAGTAC	CTGCATCTGT	CAGAAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTT	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTGT	ACATAATTG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTA ^g GT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

5

2) INFORMATION FOR SEQ ID NO: 785

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
 (B) STRAIN: ATCC 38561

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
25 TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCCT	100
GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30 GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTTCGTGCC	CATCTCCGGT	400
TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35 CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
GCCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCG	GCTTCAACGT	750
CAAGAACGTC	TCCGTCAAGG	AGGTTTCGTG	TGGAAACGTT	GCCGGTGACT	800
40 CCAAGAATGA	CCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
GTCTTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45 TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*
 448

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(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

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5  ACCACCAAGT GGTCTGAGGC CCGTTACCAG GAGATCATCA AGGAGACCTC      50
   CGGYTTCATC AAGAAGGTCG GCTTCAACCC CAAGCACGTT CCCTTCGTGC      100
   CCATCTCCGG TTTCAACGGT GACAACATGA TCGACGTCTC CACCAACTGC      150
   CCCTGGTACA AGGGTTGGGA GAAGGAGACC AAGGCCAAGG CCACCGGCAA      200
   GACCMTCCTC GAGGCCATTG ACGCCATCGA CCCCCCYAGY CGTCCCACCG      250
10  ACAAGCCCCT YCGTCTTCCC CTMCAGGATG TYTACAAGAT TGGCGGTATT      300
   GGCACGGTTC CCGTCGGTCG TGTYGAGACC GGTRCCATCA AGGGTGGCAT      350
   GGTCGTCACC TTCCCCCCCC CTGGTGTAC CACTGAGGTC AAGTCCGTCG      400
   AGATGCACCA CGAGCAGCTC GCCGAGGGTS TCCCCGGTGA CAACGTCGGC      450
   TTCAACGTCA AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GCAACGTTGC      500
15  CGGTGACTCC AAGAACGACC CCCCCAAGGG CTGCGACAGC TTCAACGCCC      550
   AGGTCATCGT CCTCAACCAC CCCGGTCAGG TCGGCGCCGG CTACGCGCCS      600
   GTCCTSGACT GCCACACTGC TCACATTGCC TGCAAGTTCT CTGAGCTCCT      650
   CGAGAAGATC GACCGCCGTT CCGGCAAGTC CATCGAGTCC GGCCCCAAGT      700
   TCATCAAGTC TGGTGACGCC GCCATCGTCA AGATGGTTCC CTCCAAGCCC      750
20

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2) INFORMATION FOR SEQ ID NO: 787

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

```

GCTCAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA      50
40  AGTTCGAGAC CCCCAGTAC CACGTCACCG TCATTGATGC CCCCAGGCCAT      100
   CGTGATTTCA TCAAGAACAT GATCACTGGT ACCTCGCAGG CTGACTGCGG      150
   TATCCTCATC ATTGCCGCCG GTACTGGTGA GTTCGAGGCT GGTATCTCCA      200
   AGGATGGCCA GACCCGTGAG CACGCTCTGC TTGCCTTCAC CCTCGGTGTC      250
   CGTCAGCTGA TCGTCGCCAT CAACAAGATG GACTCGACCA AGTACTCTGA      300
45  GGCCCGTTAC AACGAAATCG TCAAGGAGGT CTCCACCTTC ATCAAGAAGA      350
   TCGGTTTCAA CCCCAGTCC GTTCCCTTCG TCCCCATCTC TGGCTGGAAC      400
   GGTGACAACA TGTTGGAGGA GTCCTCCAAC ATGCCCTGGT TCAAGGGCTG      450
   GAAGAAGGAG ACCAAGGCTG GCGAGAAGTC CGGCAAGACC CTCCTTGAGG      500
   CCATTGACAA CATTGACCCC CCGGTCCGTC CCTCGGACAA GCCCCCTCGT      550
50  CTTCCCCTCC AGGATGTCTA CAAGATCGGT GGTATCGGCA CAGTCCCCGT      600
   CGGTCGTGTC GAGACTGGTG TCATCAAGGC TGGTATGGTC GTGACCTTCG      650
   CCCCCGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAGAT GCACCACGAG      700
   CAGCTCGTCG AGGGTGTCCC CCGTGACAAC GTCGGTTTCA ACGTCAAGAA      750
   CGTTTCCGTC AAGGATATCC GCCGTGGTAA CGTCTGCTCT GACTCCAAGA      800
55  ACGACCCCGC CAAGGAGTCT GCCTCGTTCA CCGCCAGGT CATCGTCCTG      850
   AACCACCCCG GTCAGATCGG TGCCGGTTAC GCCCCGGTTC TTGACTGCCA      900
   CACCGCTCAC ATTGCCTGCA AGTTCGCTGA GTCCTCGAG AAGATCGACC      950
   GTCGTTCCGG YAAGAAGCTC GAAGAGTCCC CCAAGTTCGT CAAGTCGGGT      1000
   GACTCCGCCA TCGTCAAGAT GGTTCCTTCC AAGCCCATGT GCGTTGAGGC      1050
60  CTACACTGAG TACCCCCCTC TTGGCCGTTT CGCC      1084

```

2) INFORMATION FOR SEQ ID NO: 788

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCTTT	100
	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAAC TAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTCGAGGCT	250
25	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCG	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCCATGGT	500
30	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACCC	GTCCTACCGA	600
	CAAGCCCCTY	CGTCTCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAAGTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTCACCT	TCGCCCCCTG	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
35	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CAGATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
40	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTGGAAGCCA	ACCCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
	TGTGCGTTGA	GGCTTTCACT	GACTACCCCC	CACTTGGTCG	TTTCGCCGTC	1150
	CGTGA					1155

45

2) INFORMATION FOR SEQ ID NO: 789

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCGTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAACTTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTTCGT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCCTCCG	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCCAAG	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCCG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCTT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCCTACTGA	CTACCCCCCA	CTTGGTGC		1138

2) INFORMATION FOR SEQ ID NO: 790

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCAGCGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCAGTA	350
	TGGTCGTAC	CTTCGCCCCC	GCTGGTGTC	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

60

2) INFORMATION FOR SEQ ID NO: 791

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Aspergillus fumigatus*
 15 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
20	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTTCGC	GAATAGGCCC	100
	CAGACTCGTG	AGCATTTGCT	GCTCGCCCGC	CAGGTTGGTG	TCCAGAAGAT	150
	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACTGGTCGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
25	ACGCCGTGAC	GACATCGGTA	AAGACAGAA	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTTCTTG	400
	ATGTCTGTCT	AGGAAGTGTT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCGAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
30	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAACT	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCGTGGTATG	GTCATTGCTG	650
	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCTGACT	GGCTTCGGTG	CCAACTACCG	750
	TCCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTCCA	800
35	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

40

2) INFORMATION FOR SEQ ID NO: 792

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

	CGTTGTGCGA	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACG	50
	GATGAAAGGA	TTTGACGTTT	CTAACATCAT	TCTAGGCCTC	AGACCAGAGA	100
60	ACATTTGCTC	CTTGCCCCGC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	150

452

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCTCA	TGTCCATTGA	400
	GGAAGTGTT	TCTATCTCTG	GTGCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGGTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTTG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35

2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50

GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGCACGC GATGTGGCAG 20

2) INFORMATION FOR SEQ ID NO: 796

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25 GGTCCAATGC CWCAACWAG A 21

30 2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT 27

45 2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

TGTTGTCCC AGCCGATCGT TT

22

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T

21

25 2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

40 GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

60 ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

15 TTGCCATTTC TGGTTTCGTT 20

20 2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

35 ACTTCAGTGG TAACACCAGC 20

2) INFORMATION FOR SEQ ID NO: 804

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

55 CCTGGGACGG CCTCTGGCAT 20

2) INFORMATION FOR SEQ ID NO: 805

60 (i) SEQUENCE CHARACTERISTICS:
456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTCCA TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

50

AAAGTGGCTT CAAAGGTTGC

20

55 2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

458

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

10 GTIACIGGIT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA 22

2) INFORMATION FOR SEQ ID NO: 814

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

40 GCIGGCACGT ACACIGCCTG 20

45 2) INFORMATION FOR SEQ ID NO: 815

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

55 TGGTGATYTT CKACRGACTT 20

60

2) INFORMATION FOR SEQ ID NO: 816

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

15

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

30

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

45 AGCCGGGCTG GATCTTCTTC

20

50

2) INFORMATION FOR SEQ ID NO: 819

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

60

460

5 2) INFORMATION FOR SEQ ID NO: 820

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C

21

25 2) INFORMATION FOR SEQ ID NO: 821

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

 (vi) ORIGINAL SOURCE:
35 (A) ORGANISM: *Trypanosoma brucei*

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A

21

2) INFORMATION FOR SEQ ID NO: 822

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: *Trypanosoma brucei*

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

15 GAGCGGTATG AYGAGATTGT 20

2) INFORMATION FOR SEQ ID NO: 824

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

30 GGCTTCTGCG GCACCATGCG 20

2) INFORMATION FOR SEQ ID NO: 825

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

45 ATGAGCARCG SAACCATCGT TCAGTG 26

50 2) INFORMATION FOR SEQ ID NO: 826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium novyi*
- (B) STRAIN: ATCC 19402

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCAG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGTATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

2) INFORMATION FOR SEQ ID NO: 828

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: 9689

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCCCTG	100
	AATTAAAAGA	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

- (i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

	ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
	GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
20	TATTGACCCA	AAAACCTGGG	AAAGTTTAAAT	GAAGAGAACA	GTACTTATAG	150
	CTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
	GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
	AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAAG	GAAATGTCAG	300
	GTAGACTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTACTTAGGA	350
25	TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
	TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

30 2) INFORMATION FOR SEQ ID NO: 830

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 444 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

45	TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
	GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
	ATTGACCCTA	AGACTGGCGA	AAGCTTAAATG	AAGAGAACAG	TTCTTATAGC	150
	TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
50	GTATCACAAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
	ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
	TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
55	AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

- (i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 456 bases

464

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTT	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40

	CCAACTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
50	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

```

10  TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT      50
    GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG      100
    CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTCAGG      150
    TTTATGAGGA AACATCAGGG ATCGGTCCAG GAGAACCAGT AGTGACTACT      200
    GGTGTGCCTT TGTCGGTCGA GTTAGGCCCCG GGCCTGATTT CAGAAATGTT      250
    TGACGGTATT CAGCGACCGC TTGATCGTTT TCAAAAAGCA ACGGACAGCG      300
15  ACTTTTTAAT CCGTGGTGTG GCTATCCCAA GTCTTGATCG AAAGGCTAAG      350
    TGGGCATTTA TTCCCAAGCT AAGTGTGGT CAAGAAGTAG TTGCAGGTGA      400
    TATTTTAGGA ACTGTGCAAG AAACAGCTGT CATTGAGCAC CGTATCATGG      450
    TTCCTTATAA AGTTTCAGGG ACCTTGTTGG CTATTCATGC AGGGGACTTC      500
    ACAGTAACAG ATACAGTTTA TGAAATTAAG CAGGAAGACG GTTCCATTTA      550
20  CCAAGGTAGC CTCATGCAGA CTTGGCCAGT TCGTCAAAGT CGCCCTGTTG      600
    CTCAAAAGCT TATCCAGTC GAACCTTTGG TTACAGGTCA ACGGGTTATT      650
    GACACCTTTT TCCCTGTTAC AAAAGGTGGT GCCGCTGCCG TTCCTGGACC      700
    ATTTGGGGCA GGAAAAACAG TTGTGCAGCA TCAAATAGCT AAATTTGCCA      750
    ACGTTGATAT TGTTATTTAT GTCGGTTGTG GGGAACGCGG CAACGAGATG      800
25  ACCGACGTTT TGAATGAGTT TCCAGAGTTA ATTGACCCAA ATACAGGCCA      850
    GTCCATTATG GAGCGCACGG TGTTAATTGC AAACACCTCT AATATGCCAG      900
    TAGCAGCGCG TGAAGCGTCG ATTTACACAG GTATTACCAT TGCCGAATAT      950
    TTCCGTGATA TGGGCTATTC TGTGGCTATC ATGGCAGACT CGACATCAGC     1000
    TTGGGCAGAA GCTCTGCGCG AGATGTCAGG ACGCCTACAA GAAATGCCTG     1050
30  GTGATGAAGG CTACCCGGCT TACTTAGGGA GTCGTATTGC CGAATATTAT     1100
    GAACGGGCTG GTCGTGTTCT GACCTTGGGA AGTCAAGAAC GTGAGGGAAC     1150
    CATTACAGCC ATCGGCGCGG TTTCTCCTCC TGGAGGGGAT ATTTTCAGAGC     1200
    CTGTCACTCA AAACACCCTT CGGATTGTCA AAGTTTTCTG GGGGCTCGAC     1250
    GCGCCTCTTG CGCAACGGCG TCACTTCCCA GCGATTAAC TGGCTGACGTC     1300
35  TTATTCATTG TATCAAGATG ATGTAGGAAG CTATATTGAC CGTAAACAGC     1350
    AATCTAATTG GTCCAACAAG GTAACTCGTG CCATGGCTAT TTTGCAGCGT     1400
    GAAGCCAGTC TAGAAGAAAT TGTACGCTTG GTGGGGCTTG ATTCACTGTC     1450
    TGAACAAGAT CGTTTGACCA TGGCTGTTGC CCGGCAAATT CGGGAGGATT     1500
    ATCTCCAGCA AAATGCCTTT GATTGCGTGG ATACCTTTAC TTCCTTTCCG     1550
40  AAACAAGAGG CCATGCTAAC CAATATTTTG ACCTTTAATG AGGAAGCCAG     1600
    CAAAGCCCTT TCTTTGGGAG CTTATTTTAA TGAGATTATG GAAGGCACTG     1650
    CTCAGGTACG CGATCGCATC GCACGCAGCA AATTTATCCC AGAAGAAAAC     1700
    TTAGAGCAGA TTAAAGGGCT TACTCAGAAG GTTACCAAAG AGATTCACCA     1750
    CGTTTTAGCA AAGGGAGGAA TTTAGATGAG CGTTCT      1786
45

```

2) INFORMATION FOR SEQ ID NO: 834

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

```

5  TATCTCACGT AAGTTTTTGC GCGGCGGTTA TATATCACTC CAGGCCCTGG 50
   CTAAGTACGC TAATACTGAC GTTACTGTCT ATGTGGGATG TGGAGAGCGT 100
   GGAAACGAGA TTGCGGAGGT GCTTAAGGAG TTCCCTGAGC TGAAGACCAA 150
   GGTGATGCG AAGGAAGTGA GCATTATGAA ACGCACTTGC TTGGTGGCCA 200
   ATACTTCAAA CATGCCAGTG GCCGCCAGGG AGGCTAGTAT CTACACTGGC 250
   ATTACCCTAT GTGAATACTT CAGGGATATG GGATACAACG CCTGTGTGAT 300
10 GGCGGATTCC ACCAGTCGTT GGGCTGAGGC TTTGCGTGAG ATATCAGGTC 350
   GTTTAGCTGA GATGCCTGCT GATTCAGGTT ATCCCGCCTA CCTTGCTTCT 400
   AGGCTTTTCGG CGTTCTATGA GCGTGCTGGT ACAGCTGAGT GTATTGGAAC 450
   ACCACTTCGT GAAGGTTTCA TTACCATTGT TGGTGCTGTA TCTCCACCA 499

```

15

2) INFORMATION FOR SEQ ID NO: 835

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

```

   TTTCTCAAGC TTTGAGTAAA TATAGTAACT CTGATGTTAT TATTTACATT 50
   GGTTGTGGAG AAAGAGGAAA TGAAATGGCA GAAGTTCTTA CAGAATTCCC 100
   TGAGCTTTAT ACTATGGTTG ATGGAAAGAA GGAGTCAATT ATGCAAAGAA 150
35 CTTGTTTAGT AGCTAATACA TCAAATATGC CTGTCGCTGC TAGAGAAGCT 200
   TCCATCTACA CTGGTATTAC ACTTTCTGAA TACTTTAGAG ATATGGGATG 250
   TAATGTTTCT ATGATGGCAG ATTCAACTTC TCGTTGGGCT GAAGCTCTTA 300
   GAGAAATTTT TGGTAGATTA GCTGAAATGC CTGCAGATTC GGGTTACCCA 350
   GCATATTTAG GCGCCAGACT TGCTTCATTC TATGAAAGAT CAGGAAGAGT 400
40 TAAATGTATG GGTTCCTCCAG ATAGAGAAGG TACAGTAACA ATTGTTGGTG 450
   CAGTTTCTCC ACCT 464

```

45 2) INFORMATION FOR SEQ ID NO: 836

3)

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

60


```

GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TC&GCTGCGG      50
CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCTTGA      100
CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC      150
GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCGCGTGAGG CCTCTATTTA      200
5  CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG      250
  CCATGATGGC TGACTCGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT      300
  TCGGGTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT      350
  CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA      400
  TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT          446
10

```

2) INFORMATION FOR SEQ ID NO: 837

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania major*
 25 (B) STRAIN: ATCC 50122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

```

TTAGTCAGGC CCTCTCCAAG TACTCCAAC TCGACTGCGT CATCTATGTC      50
30 GGCTGCGGCG AGCGCGGTAA TGAGATGGCT GAGGTGCTCA TGGATTTCCC      100
  AACTCTGACG ACCGTGATCG ATGGTCGCGA GGAGTCCATC ATGAAGCGCA      150
  CCTGCCTCGT GGCAAACACT TCGAACATGC CAGTCGCAGC CCGCGAGGCC      200
  TCTATTTACA CCGGCATCAC CCTGGCCGAG TACTACCGTG ATATGGGCAA      250
  GCATATTGCC ATGATGGCCG ACTCGACATC TCGCTGGGCC GAGGCGCTTC      300
35 GTGAGATTTT CGGTCGTCTG GCGGAGATGC CAGCCGATGG TGGCTACCCT      350
  GCCTACCTCA GCGCTCGTCT CGCCTCCTTC TACGAGCGCG CCGGCCTCGT      400
  CACCTGCATC GCGGGGCCGA AGCGCCAGGG CTCCGTCACG ATCGTCGGTG      450
  CTGTGT          456
40

```

2) INFORMATION FOR SEQ ID NO: 838

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: MOU-2
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

```

AGGCCCTCTC CAAGTACTCC AACTCCGACT GCGTCATCTA CGTCGGCTGC      50
GGCGAGCGCG GTAATGAGAT GGCCGAGGTG CTCATGGAGT TCCCGACCTT      100
60 GACGACTGTG ATTGATGGCC GTGAGGAGTG GATCATGAAG CGGACCTGCC      150

```

	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
	TTTCGGGTCTG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5	CTTAGTGCTC	GTCTTGCTC	CTTCTACGAG	CGTGCCGGCC	TCGTACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 bases
 - (B) TYPE: Nucleic acid
 - 15. (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
- (B) STRAIN: EATRO 795

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

25	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCGCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
35	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
- 50 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
55	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGACGCC	CCGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTGCGGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GA CTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTGAGTTCGC	CCAAGTCTGT	GTTCACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGCG	GTACCTGAAG	350
	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTGCGGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GA CTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

60 2) INFORMATION FOR SEQ ID NO: 842

470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

```

15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA      50
   AGTTCGAGTC GCCCAAGTCT GTGTTACGCA TCATCGACGC CCCCGGCCAC      100
   CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC      150
   CGTCCTTGTC ATTGCGTCAT CGCAGGGTGA GTTTGAGGCG GGCATCTCGA      200
20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG      250
   AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAACCT      300
   CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCG GCGTACCTGA      350
   AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC      400
   TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA      450
25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC      500
   CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC      550
   GGTATCGGCA CCGTGCCGGT CCGTCGCGTG GAGACGGGCA CGATGAAGCC      600
   CGGCGACGTG GTGACGTTTG CGCCCCCAA CGTGACGACG GAGGTGAAGT      650
   CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC      700
30 GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG AAGGACATCC GCCGTGGCAA      750
   CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA      800
   CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT      850
   GCGCCGGTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA      900
   GATCGAGTCC AAGATCGACC GCCGCTCCGG CAAGGAGCTT GAGAAGAACC      950
35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG      1000
   AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT      1050
   TGCCGTGCGT GA                                         1062

```

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

```

60 TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCAATGGCG      50
   AGTAACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
   GGTATTACTA TAAATTGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
   TTACGGTCAC GTGGACTGTC CAGGTCACTC TGATTATGTG AAGAACATGA      200

```

	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTCGTGA	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCGT	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTG	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGATCG	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

20

2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 943 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TGCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTGCGAGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCGGC	550
	ACCGGCGACA	CAACAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC GGGA	GGAGCTGAAC	AAGAAATTCG	800
	GCCGCGGCCG	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCC	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

472

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

15	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCATCT	CTTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGG	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
20	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAAG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCAGCG	AATGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
25	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGG	550
	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
30	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
	GCCGCGGCCG	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
35	GCTGGCGTAC	CCGATGCCCA	TTGACAAGGG	TCTGAAGTT		939

2) INFORMATION FOR SEQ ID NO: 846

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

55	CATTGTGGTG	GCGGCCACCG	ACGGCGTCAT	GCCGCAGACA	CGCGAGCACC	50
	TCCTGATCTG	CTCGCAGATC	GGGCTTCCGG	CGCTCGTAGG	GTTCATCAAC	100
	AAGGTGGACA	TGACGGACGA	GGACACGTGC	GACCTGGTGG	ACATGGAGCT	150
	GCGCGAGCAG	CTGGAGAAAT	ACAAGTTTCC	GGCGGAGGAG	ACGCCAATCG	200
	TGCGCGGCTC	AGCCCTCAAA	GCGTCGAGG	GCGATGCGAA	GTACGAGGAG	250
	AACATTCTCG	AACTGGTGCG	GAAGTGTGAC	GAGTGGATCC	CTGACCCGCC	300
60	GCGCAACACA	GACAAGCCTT	TCCTTATGGC	CATCGAGCAC	GTTTACGAGA	350

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCGTGA	CCGGCCGCGT	CGATCAGGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTTCGACGGT	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCGG	GACCGGCGAC	550
5	ACGACCAGTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCCTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACCGCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCATGCCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

15

2) INFORMATION FOR SEQ ID NO: 847

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania infantum*
 - (B) STRAIN: MOU

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGAACAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCGCA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCCGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTGA	AAAGGGTCTG	AAGTTCACC		939

55

2) INFORMATION FOR SEQ ID NO: 848

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

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10 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC      50
   AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG      100
   GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGCTGGA      150
   GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC      200
   TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG      250
15 GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA      300
   GCCTTTCTCT ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA      350
   AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC      400
   ACAGACGCCG AGCTGGCCGG CTTCAGCGCC AAGAAGGCGA CAGTCAAAGT      450
   GACGGGCATC GAGATGTATC ACAAGACACT CAATGAGTGC ATGCCCGGCG      500
20 ACTCTGTCCG TGTCAGCATC GTCGGTACCG GTGACACGAC CAGCTTATCC      550
   AAGGATAATG TTGAGCGCGG TATGGTAATG GCGGCAACGG GTAGCACGAA      600
   CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG      650
   GTGGCCGCCA CACCGGGTTC AGCCCCACT ACCGCCCGCA GCTCTTCTTC      700
   CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA      750
25 CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA      800
   AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTTG CTGCATGCCA      850
   GGCGATAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA      900
   CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CCG                      933

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30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

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CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
50 TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
   CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
   CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
   TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AGTGGATCCC      300
   CGACCCGCCG CGCAACACAG ACAAGCCTTT CTTATGGCC ATCGAGCACG      350
55 TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
   GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG      450
   CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA      500
   CGCTGAGCGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCGGC      550
   ACCGGCGACA CGACCAGTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT      600
60 AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650

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	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCA S CCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCTCT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCCGGT	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCCGA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
45	GCGTACCCGA	TGCCCCATT				918

2) INFORMATION FOR SEQ ID NO: 851

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 60 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
5	GCGAGCATCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGG	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
10	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGTCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGGC	550
15	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGCGGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCG	800
20	GCCGCGGCCG	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAGAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 852

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 912 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tarentolae*
 - (B) STRAIN: MOU-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

	TCATTGTGGT	GGCCGCCACC	GACGGCGTCA	TGCCGCAAAC	ACGGGAGCAC	50
	CTTTTGATCT	GCTCGCAGAT	CGGGCTGCCG	GCGCTCGTAG	GGTTCATCAA	100
	CAAAGTGGAC	ATGACAGACG	AAGACACGTG	CGACCTGGTA	GACCTGGAGG	150
45	TGCGTGAGCA	GCTGGAGAAG	TACAAGTTTC	CGGCAGAGGA	AACACCAATC	200
	GTGCGTGGCT	CGGCCCTCAA	GGCCGTTGAG	GGCGATGCAA	AGTACGAGGA	250
	GAACATCCTC	GAAGTGGTGC	GGAAGTGCGA	CGAGTGGATC	CCAGACCCGC	300
	CACGCAATAC	GGACAAGCCT	TTCTTTATGG	CCATTGAACA	CGTGTACGAG	350
	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
50	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GAACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATTGTGG	GCACTGGYGA	550
	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTACTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
55	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCACTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAAGTCA	ATAAGAAATT	CGGCCGCGGC	800
	CCCAGGAGG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
60	ACCCGATGCC	TA				912

2) INFORMATION FOR SEQ ID NO: 853

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

20 ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA 50
 CCTGCTTATT TGTTTCGAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA 100
 ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTTGAA 150
 ATGGAGGTAC GTGAACTTTT GGAGAAGTAC AAGTTCCCTG CGGAGGAGAC 200
 GCCATTTGTG CGGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA 250
 25 ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC 300
 GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT 350
 TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTTGTGAGC GGGCGTGTGG 400
 ACCAGGGGCA GTTGAAGGTC GGCGCAGATG CAGAACTTTC CGGGTTTAGC 450
 GCAAAGAAGC TGACGGTGAA GGTGCTAGC ATCGAAATGT ACCATAAAAT 500
 30 TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGCGAAG ATCGTTGGCA 550
 GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA 600
 CTCTCCGCAC CAGGTGCAAC GACACTGTTC AACAAGGTCC GCGCGCAGGT 650
 GTACGTGTTG ACAAAGGAAG AAGGCGGTCG TCACACAGCC TTTAGTCCTC 700
 ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT 750
 35 AACTTCCCGG AAAGCGAGAA GCTTGCAAGG GAGCTGAACA AAAAGTATGG 800
 CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG 850
 AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC 900
 CTTGCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG 936

40

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG 50
 AGCACCTGCT TATTTGTTTC GAGATTGGCC TTCCTGCTCT TGTATGCTTT 100
 60 ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT 150

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCCTTATG	GCCATTGAGC	350
5	ACGTTTTTGA	GGTTGGAAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGACT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTCGAAG	GAAAATGTGG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAAC TTC	CCGGAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 937 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma cruzi*
 - (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGACCTT	GCTTATTTGT	TCGAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGA	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATTCCCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCCGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCT	AAGGAAAAAT	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCTGTA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCCCT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

- 60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

CTTATTATGG AGCTGATCAA CAACGTCGCG AAGAAGCACG GTGGTTTCTC 50
 15 CGTGTTTCGCC GGCCTCGGCG AGCGCACCAG GGAGGGCAAC GAGCTGTACC 100
 ACGAGATGAT GGAGACCGGC GTCATCAAGC GCCGCCAGCT GGATGACGGC 150
 ACGTTCGACT TCTCCGGCTC CAAGGCCGCG CTGGTGTACG GCCAGATGAA 200
 CGAGCCGCCA GGTGCCAGGG CGCTGTGTGC CCTCACTGGC CTGACGGTGG 250
 CCGAGTACTT CCGTGATGAG GACGGCCAGG ACGTGCTGCT CTTTCATCGAC 300
 20 AACATCTACC GTTTCACCCA GGCTGGTTCT GAGGTGAGTG CCCTTTTGGG 350
 GCGCATCCCG TCCGCCGTCG GTTACCAGCC GACCCTCGCC ACCGACCTTG 400
 GCGCGCTGCA GGAGCGTATC ACGACGACCA ACAAGGGCTC CATCACCTCC 450
 GTGCAGGCCG TCTACGTGCC GGCCGACGAT ATCACCAGCC CGGCGCCTGC 500
 GACCACCTTC ACCCATCTGG ACGCGACCAC TGTGCTCTCC CGTTCCATCG 550
 25 CCGAGCTGGG TATCTACCCC GCCGTCGACC CGCTCGACTC CACCTCGCGT 600
 ATGCTGTCCG CGAACATCGT CGGCGAGGAG CAGTACAACG TGGCGCGTGG 650
 CGTGCAGAAA ATACTGCAGG ACTACAAATC GCTGCAGGAT ATCATCGCCA 700
 TCCTGGGTAT GGACGAGCTG TCTGAGCAGG ACAAGTTCGT CGTCGCGCGT 750
 GCGCGCAAGG TTCAGCGTTT CCTATCCCAG CCCTTCCAGG TGGCTGAGGT 800
 30 ATTCACCGGC AAGCCCGGAC GTTTCGTCTGA GCTGCAGGAC ACCATCAGCG 850
 GCGTCAAGGA GATTTTGGAC GGCGAGTGCG ACGACATG 888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

TGATTATGGA ATTGATCAAC AATGTCGCCA AGAAACACGG TGGGTTCTCC 50
 GTGTTTCGCTG GTGTTGGTGA ACGTACGAGG GAAGGTAACG AACTGTACCA 100
 TGAAATGATG GAAACGGGTG TCATCAAGCG CCGTCAACTG GAAGACGGAA 150
 CATTGACTT CTCGGGCTCT AAAGCTGCTT TGGTGTACGG ACAAATGAAC 200
 55 GAACCACCAG GTGCTAGAGC CCGTGTGCA CTCACGGGAT TGACCGTTGC 250
 CGAGTATTTT CCGTATGAAG AGGGGCAGGA TGTGCTACTC TTCATCGATA 300
 ACATCTACCG TTTCACCCAG GCCGGTTCCG AAGTGAGTGC GCTGTTAGGA 350
 AGAATTCCAT CCGCCGTGGG TTATCAACCT ACATTGGCCA CTGATCTCGG 400
 AGCACTCCAG GAACGCATTA CTACAACCAA CAAGGGTTCG ATTACATCAG 450
 60 TCCAGGCAGT ATACGTCCCA GCCGATGATA TCACTGATCC CGCTCCAGCT 500

480

ACCACTTTCT CGCACTTGGA TGCCACTACA GTGCTTTCTC GTTCAATTGC 550
 GGAGTTGGGT ATTTACCCTG CGGTGACCCC GCTTGACTCA ACGTCACGTA 600
 TGCTGTCGGC CAACATTGTA GGACAGGAAC AGTACGATGC CGCACGTGGT 650
 GTACAGAAAA TTTTACAGGA CTACAAATCA CTGCAGGATA TCATTGCCAT 700
 5 TCTGGGTATG GACGAGCTGT CTGAGCAGGA CAAGTTCGTT GTAGCACGCG 750
 CCCGTAAGGT ACAGCGTTTC CTGTCTCAGC CGTTCCAAGT GGCTGAGGTG 800
 TTCACCGGCA AGCCTGGGAG GTTCGTTGAA CTACAGGATA CCATCAGCGG 850
 TGTCAAGGAA ATCTGGAAGG TGAGTGTGAC GATA 884

10

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

TGGAAGTATG TAATAATGTG GCCAAAAAGC ATGGCGGTTA CTCTGTTTTT 50
 GCAGGTGTAG GTGAAAGGAC GAGGGAGGGT AATGAATTGT ACCATGAAAT 100
 30 GATGGAGACA GGTGTTATAA AGAAAAAGGC ACTAGGTGGT GGGAAAGTTTG 150
 ATTTCAAGTGG ATCTAAAGCA GCGCTGGTCT ATGGACAAAT GAACGAGCCA 200
 CCTGGGGCCC GTGCTAGAGT GGCCTAAGT GGATTAACAG TCGCAGAATA 250
 TTTCCGTGAC GAACAAGGAC AAGACGTGTT GTTGTATTATT GATAATATTT 300
 ACCGATTTAC TCAGGCAGGG TCTGAGGTTT CAGCCTTGCT AGGCCGTATA 350
 35 CCTTCAGCTG TGGGATACCA GCCTACATTG GCAACAGATC TTGGCTGTTT 400
 ACAAGAACGA ATTACTACGA CCAATCTGG TTCAATCACC AGTGTACAAG 450
 CTGTGTATGT GCCAGCAGAT GATATTACTG ATCCAGCGCC TGCCACAAC 500
 TTTACTCACT TGGACGCTAC TACTGTACTT AGCAGGCCAA TTGCTGAACT 550
 CGGTATTTAT CCAGCGGTAG ACCCGTTGGA TTCAACAAGC CGTATGCTAA 600
 40 GCGCGAACAT TGTGGGAAAT GAACACTATA GTGTAGCCCG TTCCGTGCAG 650
 AAGATACTGC AAGATTACAA ATCGCTTCAG GACATTATTG CCATTTTGGG 700
 TATGGATGAA CTGTCGGAAC AAGACAAAAA TATAGTAGCC CGAGCAAGGA 750
 AGATGCAAAG GTTCTTATCA CAGCCATTCC AAGTGGCGGA AGTTTTTACT 800
 GGTAACCCGG GAAGATTTGT GGAATTGGAA GATACAATTG CCGGGGCACG 850
 45 AGATATAATT GCGGGTAATT G 871

2) INFORMATION FOR SEQ ID NO: 859

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania guyanensis*
 481

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

5	TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
	CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
	GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
	GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
	GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
10	CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
	ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
	TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGG	GGTGCCGGTG	TGGGCAAGAC	400
	TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
	TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
15	TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
	GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
	GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
	GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
	GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
20	ACCAGCCGAC	GCTTGCGGAG	GATCTTGCCA	TGCTGCAGGA	GCGCATTACG	800
	TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
	GGATGATATC	ACGGACCCCG	CGCCC GCGAC	GACGTTCTCG	CACCTGGACG	900
	CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
	GTGAACCCGC	TGGAGTGCGC	GTGCGGCATC	ATGGACCCCG	ATGTGATCGA	1000
25	CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
	ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
	GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
	GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
	ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
30	TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 860

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Leishmania mexicana*

(B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

50	CTCGGAGGGC	GTCCCCGCCC	TGCTGACGGC	GCTGGATGTG	ACGGAGGACC	50
	TTGGCCGCGA	TGAGCCGCTG	ACGCTGGAGA	TCGTGCAGCA	CCTGGACGCG	100
	AACACCGGCC	GCTGCATTGC	GATGCAGACG	ACGGACCTGC	TGAAGCTGAA	150
	GTCGAAGGTT	GTGTGACCGG	GCGGCAACAT	CTCTGTGCCG	GTGGGCCCGTG	200
	AGACGCTGGG	CCGCATCTTC	AACGTGCTGG	GCGACGCGAT	CGACCAGCGC	250
55	GGCCCCGTGG	GTGAGAAGAT	GCGCATGGCG	ATCCACGCCG	AGGCCCCGAA	300
	GCTGGCGGAT	CAGGCCGCGG	AGGACACGAT	CCTGACGACC	GGCATCAAGG	350
	TGATCGACCT	GATTCTGCCC	TACTGCAAGG	GTGGCAAGAT	CGGCCTGTTT	400
	GGCGGCGCCG	GTGTGGGCAA	GACCGTGATC	ATCATGGAGC	TGATTAACAA	450
	CGTCGCGAAG	GGCCACGGTG	GTTTCTCGGT	GTTTGCCGGC	GTTGGCGAGC	500
60	GCACGCGCGA	GGGCACGGAC	CTGTACCTGG	AGATGATGCA	GTCGAAGGTG	550

	ATTGACCTGA	AGGGCGAGTC	GAAGTGCGTG	CTTGTGTACG	GGCAGATGAA	600
	CGAGCCCCCG	GGTGCGCGCG	CGCGCGTTGC	GCAGTCTGCG	CTGACGATGG	650
	CGGAGTACTT	CCGAGACGTG	GAGGGCCAGA	ATGTGCTGCT	GTTTCATCGAC	700
	AACATCTTCC	GCTTCACGCA	GGCGAACTCC	GAGGTCTCTG	CGCTGCTGGG	750
5	CCGCATTCCG	GCCGCCGTGG	GCTACCAGCC	GACGCTTGCG	GAGGATCTTG	800
	GTATGCTGCA	GGAGCGCATC	ACGTCGACGA	CGAAGGGGTC	GATCACGTCC	850
	GTGCAGGCCG	TGTACGTGCC	TGCGGATGAT	ATCACGGATC	CGGCGCCCGC	900
	GACGACGTTT	TGCGACCTGG	ACGCGACGAC	TGTGCTGGAC	CGCGCGGTGG	950
	CGGAGTCGGG	GATCTACCTT	GCCGTGAACC	CGCTGGAGTG	CGCGTCGCGT	1000
10	ATCATGGACC	CCGATGTGAT	CGACGTGGAC	CACTACAACG	TTGCGCAGGA	1050
	TATCGTGACG	ATGCTGACCA	AGTACAAGGA	GCTGCAGGAT	ATCATTGCGG	1100
	TGCTTGGTAT	CGACGAGCTG	AGCGAGGAGG	ACAAGGTCGT	GGTGGACCGC	1150
	GCGCGCAAGG	TGACCCGGTT	CCTGTGCGAG	CCGTTCCAGG	TTGCGGAGGT	1200
	GTTACAGGGC	ATGACGGGCC	AC			1222

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2) INFORMATION FOR SEQ ID NO: 861

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 50129

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	CGATGAGCCG	50
35	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACCG	GCCGCTGCAT	100
	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	GTTGTGTGCA	150
	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	GGGCCGCATC	200
	TTCAACGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	TGGGCGAGAA	250
	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	GATCAGGCCG	300
40	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	CCTGATTCTG	350
	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	CCGGTGTGGG	400
	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	AAGGGCCACG	450
	GTGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	CGAGGGCACG	500
	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	TGAAGGGCGA	550
45	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	GAACGAGCCC	CCGGGTGCGC	600
	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	CTTCCGCGAC	650
	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	TCCGCTTCAC	700
	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	CCGGCCGCCG	750
	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
50	ATCACGTGCA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
55	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	GGTGTTCACG	GGCATGACGG	1200
	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

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2) INFORMATION FOR SEQ ID NO: 862

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
20	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTCGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCATC	TTCAAYGTTT	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
25	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
30	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	850
35	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
40	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTGCG	CAGCCGTGCC	AGGTTGCGGA	GGTGTTCACG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
	TGGCCTGCTG	ATGGG				1265

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2) INFORMATION FOR SEQ ID NO: 863

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGGG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCGG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTG	GGCCGCGAGC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTGCG	GCCAGGTTGG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAACG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTGCG	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGGAGCG	CGCGGTGCGC	GGTGCGTTCC	TGATGCCCGT	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACGG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCAG	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTGCGG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCC	900
20	ATCAACCCGC	ACACGGACTT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCGG	TGCCGGCGTC	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: LVH/75/USAMRU-K/18
 (C) ACCESSION NUMBER: extracted from U10562

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

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	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTCGA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCGTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
	CTCTGCGCAG	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACTTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCGGTGGTAT	TGGCACCGTG	750

	CCC GTTGGT C	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGYGAC	800
	GTTTGCCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
	ACGAGCAGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
	CGACCGTCCG	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	GAGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCT	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

15

2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

30

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTTCGAA	ACCCCAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTGG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
35	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTCAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCTGTGC	CATTTCTGGT	TTCTGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
40	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTAC	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
45	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTTCTTGCA	AATTCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
50	CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
	GA					1052

55

2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid

60

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 35552

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20	TTCGGTGGCG	CTGGTGTAGG	TAAACAGTA	TTAATTC AAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

30

2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
(B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

	AAGGTATTTCG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
	ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50	CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
	ATGGTGCCAG	TCGGTAAAGC	AACCCTGGGT	CGCATCATGG	ACGTGCTGGG	200
	TAACCCGATC	GACGAATGCG	GCGCGGTCGC	TCACGACCAG	ATCGCTTCGA	250
	TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTCGCCATC	GCAAGATCTG	300
	CTGGAAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCGT	TCGCCAAGGG	350
55	CGGTAAAGTC	GGTCTGTTTC	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
	TGATGGAAC	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
	TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
	TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60	GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	CCGCTTCACC	CTGGCCGGTA	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 43867

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
25 CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
30 CACCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
35 TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCACAAT	TCTATTTCGG	700
TACTACTGAC	GTAACGGTG	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
40 TTATGCCTGG	CGATAACGTT	GAAATGGA			778

2) INFORMATION FOR SEQ ID NO: 869

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R689

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
60 GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

488

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCTGACT	TATTGTGAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAAACTGCT	AAAACAACTG	TAACCTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTG	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 644 bases
- (B) TYPE: Nucleic acid
- 20 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: R754

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTGAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCCTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AACTGCTAA	AACAACGTGA	ACTGGTGTG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 637 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
- (B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTT	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACGTGTA	CTGGTGTGTA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AACTGCTAA	AACAACGTGA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

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GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAAGT TCGTGACCTA TTGTCTGAAT      150
10 ATGACTTCCC AGGCGACGAT GTTCTGTAA TCGCCGGTTC TGCTTTGAAA      200
GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
TGCAGTTGAC GAATACGTTC CAACTCCAGA ACGTGATACT GACAAACCAT      300
TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
GCTACAGGCC GTGTTGAACG TGGACAAAGT CGCGTTGGTG ATGAAGTAGA      400
15 AATCGTTGGT ATTGCTGACG AAAGTGTCTA AACAAGTGTG ACAGGTGTTG      450
AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT      600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT C              641
20

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2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 35 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

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ACCAGCATTG GTAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
40 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG      200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC      250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
45 TACAGGCCGT GTTGAACGTG GGCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG      400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
CTCCAGGTTT AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
50 TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG      600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTG GTTAACTTAC      650
CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A              681

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55

2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 bases
 60 (B) TYPE: Nucleic acid

491

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: R591

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTC	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTA AAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCGGT	ACTACTGACG	650
25	TAAC TGGTGT	TGTAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAATTCC	250
50	AGAACGTGAT	TCTGACAAAC	CATTATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAAC TGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTGTC	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTA ACTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

60

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
20	ATCTTATTAT	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
	GTAATCGCTG	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	250
	ACAAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	300
25	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
	AAACAACTGT	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTG	CACGTGAAGA	550
30	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
	TGACGTAAC	GGTGTGTGTA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
35	CTGGCGACAA	CGTTGAAATG				770

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

	TTGTATTCTT	AAACAAAGTT	GACATGGTAG	ACGACGAAGA	ATTATTAGAA	50
55	TTAGTTGAAA	TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	100
	TGACGATGTA	CCTGTAATCG	CTGGTTCTGC	ATTAAAAGCA	TTAGAAGGCG	150
	ATGCTGAATA	CGAACAAAAA	ATCTTAGACT	TAATGCAAGC	AGTTGATGAT	200
	TACATTCCAA	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	250
	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCCGTG	300
60	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	CATCGGTATG	350

	CACGAAACTT	CTAAAACAAC	TGTTACTGGT	GTAGAAATGT	TCCGTAAATT	400
	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	TTACGTGGTG	450
	TTGCACGTGA	AGACGTACAA	CGTGGTCAAG	TATTAGCTGC	TCCTGGTTCT	500
	ATTACACCAC	ACACAAAATT	CAAAGCTGAA	GTATACGTAT	TATCTAAAGA	550
5	TGAAGGTGGA	CGTCACACTC	CATTCTTCAC	TAACTATCGC	CCACAATTCT	600
	ATTTCCGTAC	TACTGACGTA	ACTGGTGTG	TAAACTTACC	AGAAGGTACA	650
	GAAATGGTTA	TGCCTGGCGA	CAACGTTGAA	ATGACAGTTG	AATTAATCGC	700
	TCCAATCGCT	ATCGAA				716

10

2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

	CGGTCCTATG	CCTCAAACTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	CGGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
30	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCTGTGACC	TATTGCTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCCGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
40	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

2) INFORMATION FOR SEQ ID NO: 880

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60	CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCATG	CCGCAGACCC	50
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	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCCTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAGTGGT	150
	CGAGATGGAA	GTTCGCGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCTTGATGC	350
	CGATCGAAGA	CGTGTTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAGAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTA	GTGCTGTCCA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

495

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTCTG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTG	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTAAGTTGTC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TTCGTGAAGT	ATTATCAGAA	150
	TACGATTTC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAATCCAG	AACGTGATAC	TGACAAACCA	300
	TTCAATGATG	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTGTAAC	GTGGTGAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACGTG	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

55

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: R575

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
15	TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
20	GTTGGTATTA	AAGACGAAAC	ATCTAAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

25

2) INFORMATION FOR SEQ ID NO: 885

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R492

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

	TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTTCCT	50
45	TACATCGTTG	TATTCTTGAA	CAAAGTAGAC	ATGGTTGATG	ACGAAGAATT	100
	ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
	TCCCTGGTGA	CGATGTTTCCT	GTAGTTGCTG	GATCAGCTTT	GAAAGCTCTA	200
	GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250
	TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTTCATGA	300
50	TGCCAGTTGA	AGACGTGTTC	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
	GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAAGTTGT	400
	TGGTATTGCT	GAAGAAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
	TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
	CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
55	ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
	TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

60 2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

15	CGGCCCAATG	CCTCAAAC	GTGAACAC	CCTATTGTCT	CGTCAAGTTG	50
	GTGTTCTTA	CATCGTTG	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	100
	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	150
	ATACGAATTC	CCTGGTGACG	ATGTTCTGT	AGTTGCTGGA	TCAGCTTTGA	200
20	AAGCTCTAGA	AGGCGACGCT	TCATACGAAG	AAAAAATTCT	TGAATTAATG	250
	GCTGCAGTTG	ACGAATACAT	CCCAACTCCA	GAACGTGACA	ACGACAAACC	300
	ATTCATGATG	CCAGTTGAAG	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	350
	TTGCTACAGG	TCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAGTTGTTG	GTATTGCTGA	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	450
25	TGAAATGTTT	CGTAAATTGT	TAGACTACGC	TGAAGCTGGA	GACAACATTG	500
	GTGCTTTACT	ACGTGGTGT	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	550
	TTAGCTAAAC	CAGGTACAAT	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	600
	ATACGTGTTG	ACAAAAGAAG	AAGGTGGACG	TCATACTCCA		640

30

2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

	ATCCTGGTTT	GCTCCGCAGC	TGACGGCCCA	ATGCCACAGA	CCCGCGAGCA	50
	CATCCTGCTG	GCCCGCCAAG	TTGGCGTTCC	ATACATCATC	GTGTTCTTGA	100
50	ACAAGTGCGA	CCTGGTTGAC	GACGCAGAAC	TGCTGGAACT	GGTCGAAATG	150
	GAAGTGCGTG	AATTGCTGTC	GAAATACGAG	TTCCCAGGCG	ACGACGTACC	200
	AATCATCAAG	GGTTCGGCAC	GTATGGCGCT	GGAAGGCAAA	GAAGGCGAGA	250
	TGGGCGTTGA	CGCCATCATG	CGTCTGGCCG	ATGCACTGGA	CAGCTACATC	300
	CCTACGCCAG	AGCGCGCAGT	CGATGGCGCC	TTCTGTATGC	CAGTGGAAGA	350
55	CGTGTTCTCG	ATCTCGGGTC	GCGGTACCGT	TGTGACCGGT	CGTATCGAGC	400
	GCGGCGTGAT	CAAGGTCGGC	GAGAGATCG	AAATCGTCGG	CATTATCGAC	450
	ACCGTCAAAA	CCAATTGCAC	CGGCGTGGAA	ATGTTCCGCA	AGCTGCTGGA	500
	CCAGGGTCAA	GCCGGCGACA	ACGTTGGTCT	GCTGCTGCGC	GGCACCAAGC	550
	GTGAAGACGT	ACAGCGTGGT	CAGGTTCTGG	CCAAGCCAGC	GTCGATCAAG	600
60	CCGCACAACC	ACTTCACCGG	CGAGATCTAC	GTTCTGTCTGA	AAGATGAAGG	650

CGGCCGTCAC	ACCCCGTTCT	TCAACAACATA	TCGTCCACAG	TTCTACTTCC	- 700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

5

2) INFORMATION FOR SEQ ID NO: 888

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R503

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

25	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAAATACGA	150
	TTTCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCCA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTCAT	300
30	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGCGC	GACGTCACAC	TCCA		634

40 2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55	TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
	TTGCTCTGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
	GCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTACTCGTGA	150
	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTCAGCTCG	200
60	AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTCG	GACAGATGAA	CGAGCCCCCC	250

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Penicillium marneffei*
- (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTCCGGT	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTACAG	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCTGT	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
	TTCCATCACC	TCCGTC				466

35

2) INFORMATION FOR SEQ ID NO: 891

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Paecilomyces lilacinus*
- (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTG	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTGCGCCG	GTACTTCCGT	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

500

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

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2) INFORMATION FOR SEQ ID NO: 892

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Penicillium marneffei*
- (B) STRAIN: ATCC 58950

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAAC	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTTCAT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCGGT	CAGATGAACG	AGCCCCCGG	TGCCCCGTGCC	250
CGTGTGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
CCGTTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCGGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

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2) INFORMATION FOR SEQ ID NO: 893

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1208 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: ATCC 14285

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
GAGGTCCCCG	AGTTCCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTGGCA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
AGACCTCTGT	CATTGAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTT	450

501

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCCTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCTGA	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCTTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGA	ACT	TATTGTA	AAGC	CGCCCTC	TTT	ATGCATT	GAG	GGTGA	AATAAG	50
	AAGGCTG	AACA	GGTAATA	GAGAA	CAACATT	GGCC	AAGGCTC	CACG	GTGGT	TACTC	100
	CGTGTT	CACT	GGTGT	CGGTG	AGCGT	ACCCG	TGAAG	GAAAC	GATCT	GTACC	150
	ATGAAAT	GCA	GGAAAC	CCGC	GTCAT	CCAGC	TTGAT	GGCGA	GTCTA	AGGTC	200
40	GCCCTT	GTGT	TCGGT	CAGAT	GAACG	AGCCC	CCTGG	AGCCC	GTGCC	CGTGT	250
	CGCTCT	TACT	GGTCT	TACCG	TTGCC	GAATA	CTTCC	GTGAC	GAGG	AGGGCC	300
	AAGATG	GTAC	GCCTTT	TTTAC	TCTTCT	TATT	CTTCG	GGTTCG	GA	TACAGAA	350
	CTAAC	CTGCT	CCAGT	GCCTT	C		TAACAT	TTTTC	CGTTT	CACAC	400
	AAGCC	GGTTC	TGAGG	TGTCT	GCCTT	GGCTT	GACGT	ATTCC	CTCTG	CCGTC	450
45	GGTTAC	CAGC	CCACT	CTCGC	CGTCG	ACATG	GGTGG	TATGC	AGGA	ACGTAT	500
	CACAAC	CACC	AACAAG	GGTT	CCATT	ACTTC	CGTG				534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*

(B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

5 CAAGGCTCAC GGTGGTTACT CCGTCTTCAC TGGTGTCCGT GAGCGTACCC 50
 GTGAGGGTAA CGATCTGTAC CACGAAATGC AGGAGACCTC GGTCATTCAG 100
 CTCGAGGGCG AGTCTAAGGT GGCCCTGGTC TTTGGTCAGA TGAACGAGCC 150
 CCCGGGTGCT CGTGCCCGTG TCGCTCTTAC TGGTCTTACC GTCGCCGAGT 200
 10 ACTTCCGTGA CCAGGAGGGT CAGGATGGTT AGTTCTCGTC CACTCATGCC 250
 GAAACATGTG CGTGTTCCGA GGCTAATCAA CGTGCCAGTG CTGCTTTTCA 300
 TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCCGAGGT GTCTGCCCTG 350
 CTGGGTCGTA TCCCCTCTGC CGTCGGTTAC CAGCCCACCC TCGCCGTCGA 400
 CATGGGTGGC ATGCAGGAGC GTATCACCAC CACCAAGAAG GGCTCTAT 448

2) INFORMATION FOR SEQ ID NO: 896

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*

(B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

ATTCAGGAGC TGATTGTAAG TTGCCAATCC ATGAACTGGA GATTTGGTGT 50
 35 GACCCATAGA ACTAACAAAT TATTTAGAAC AACATCGCCA AGGCTCACGG 100
 TGGTTACTCC GTCTTCTGTG GTGTCGGTGA GCGTACTCGT GAGGGTAACG 150
 ATCTGTACCA CGAAATGCAG GAGACTGGTG TCATCCAGCT CGAGGGTGAC 200
 TCCAAGGTCG CTCTGGTCTT CGGTCAGATG AACGAGCCCC CGGGTGCCCG 250
 TGCCCGTGTC GCCCTTACCG GTCTGACCAT TGCCGAGTAC TTCCGTGACG 300
 40 AGGAGGGTCA GGACGTGCTG CTCTTCATTG ACAACATTTT CCGTTTCACC 350
 CAGGCCGGTT CTGAGGTGTC TGCCCTTCTG GGTCGTATCC CCTCTGCCGT 400
 CGGTTACCAG CCCACTCTGG CCGTCGACAT GGGTGGTATG CAGGAGCGTA 450
 TTACCACCAC CACCAAGGGT TCCATTACCT CCG 483

2) INFORMATION FOR SEQ ID NO: 897

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*

(B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAGTACC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCAGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Penicillium marneffe*
- (D) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTTCA	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCTCTGG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCCTTT	GTTCCCTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCTTGG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTCACCT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCCTT	1200
	CCAAGCCCAT	GTGTGTTGAG	GCTTTACCCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCCGCGTTC	GCGAGTAAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

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2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAACTGCCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCTTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCCGTGGTAT	CGGAACGTGT	650
45	CCTGTCGGCC	GTATCGAGAC	TGGTGTCTTC	AAGCCCCGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCCGCTCTG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
55	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCC	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

(i) SEQUENCE CHARACTERISTICS:

505

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
15	GTTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
	CGAGACTGGT	CGCAATTTCC	ACGTGCTAA	CGTGCTTGAA	CAGACGCTCC	150
	CGGCCACCGT	GACTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCTG	200
	ACTGCGCTAT	CCTCATTATC	GCTGCCGGCA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
20	CGGTGTTAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
	GGTCTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
	TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
25	CTTGAGGCCA	TCGACTCCAT	CAGACCCCCC	AAGCGCCCCA	GCGACAAGCC	600
	CCTCCGCCTT	CCCCTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
	TCCCTGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCCG	CATGGTCGTG	700
	ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
	CCACGAGCAG	CTCTCCGAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
30	TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
	TCCAAGAACG	ACCCCCCTCT	GGGTGCCGCT	TCTTTCGATG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGGTCGGTGC	TGGCTACGCC	CCCGTCCTCG	950
	ACTGCCACAC	CGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
	ATCGACCGCC	GTACCGGCAA	TCTGTGTCAG	TCCGCCCCCA	AGTTCATCAA	1050
35	GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
	TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32075

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

55

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTTCGAGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
60	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCCTGTCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCCTCAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

(B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTTCATCGC	GATTTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTCGG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCCG	CATGGTCGTC	ACCTTTGCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCCG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTGCGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

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2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1366 bases

60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 58950

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

	CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
	TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
	GATTTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
15	TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
	ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCT	CGGTGTCCGT	250
	CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
	TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
	GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
20	CGGATACAAC	CCTAAGAACG	TTCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
	GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCCTGGTA	CAAGGGTTGG	500
	GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
	CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCT	600
	CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTCAC	650
25	AGCCCCCTCCG	TCTTCCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
	ACGGTTCCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
	TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
	TGCTAACTTG	ACACTCAGCG	CTCCCCGCCA	CGTCACCACT	GAAGTCAAGA	850
	GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
30	GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCGTGGTAA	950
	CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
	ACGCCCAGGT	CATCGTCCTC	AACCACCCCC	GTCAGGTCGG	TGCTGGTTAC	1050
	GCCCCAGTCC	TCGATTGCCA	CAC TGCCCA	ATTGCTTGCA	AGTTCGCTGA	1100
	GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
35	CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCCCTTCC	1200
	AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCTCCTC	TCGGTCGTTT	1250
	CGCCGTTTCG	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
	TTCTCCTCCG	TCTTCCATAT	ATATTTTTC	AGTTATATGT	GACTAACCAC	1350
	AAATCACGGG	AATAGC				1366

40

2) INFORMATION FOR SEQ ID NO: 904

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*
(B) STRAIN: ATCC 26425

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

	CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GACTCGTGAG	50
60	CATCTGCTGC	TCGCCCGCCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100

508

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCTG	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCAC	TCCGACGAGT	CGTGTGCCCT	GTACTGGCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCG	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTCTCTCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCCG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTTCT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800
	ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCGCCGTA	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
	CCGGTCAGCG	CTTCAAC				967

55

2) INFORMATION FOR SEQ ID NO: 906

(i) SEQUENCE CHARACTERISTICS:

60

509

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

	TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
15	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
	CCCACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
20	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCGTG	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
25	GGTGTAAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTAAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
	CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCCGGTGAC	AACGTCGAGA	800
30	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCGTCAGG	TCGGTGTCCA	150
	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCCTGAGA	200
55	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TTGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
	TTCCTCATGT	CTGTCGAGGA	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
60	TGCCTCCGGC	CGTGTGCAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACCTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTTCG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Alternaria alternata*
- (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTGCTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTCAGAAG	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAATCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCGG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTCC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCAGG	600
	CAAGTCAAGG	CTCACAAGAA	GTTCCTTGTC	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAA	700
	TGTTTCATCCG	AACTGCCGAT	GAATCCTGCG	CACCTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

50 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

```

5      CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
      AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG      100
      CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT      150
      CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT      200
10     TGGAAATGCG TGAACCTTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC      250
      CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA      300
      GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA      350
      TCCCCACCCC CCAGCGTGAC CTTGACAAGC CTTTCTTGAT GTCCGTTGAG      400
      GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCACTCTG GTCGTGTTGA      450
15     GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA      500
      AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT      550
      TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT      600
      CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA      650
      CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT      700
20     GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT      750
      CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT      800
      GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT      850
      CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC      900
      ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G          931
25

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2) INFORMATION FOR SEQ ID NO: 910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

```

45     CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
      AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG      100
      CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT      150
      CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT      200
      TGGAAATGCG TGAACCTTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC      250
      CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA      300
50     GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA      350
      TCCCCACCCC CCAGCGTGAC CTTGACAAGC CTTTCTTGAT GTCCGTTGAG      400
      GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCACTCTG GTCGTGTTGA      450
      GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA      500
      AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT      550
55     TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT      600
      CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA      650
      CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT      700
      GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT      750
      CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT      800
60     GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT      850

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CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

35

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

50 GACGGYSYCA TGCKCAGAC

20

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

5

GAARAGCTGC GGRCGRTAGT G

21

10 2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

25

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

40

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

55

2) INFORMATION FOR SEQ ID NO: 918

(i) SEQUENCE CHARACTERISTICS:

60

514

- (A) LENGTH: 1391 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCCGCGGTG	50
15	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGA AACCAT	CTCTACCGGT	TCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTC	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTTCGTCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTTTAA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTGCGATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCIGART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

15

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

30

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

45 TARAAYTTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

60

5 2) INFORMATION FOR SEQ ID NO: 924

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20

2) INFORMATION FOR SEQ ID NO: 925

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35

2) INFORMATION FOR SEQ ID NO: 926

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50

2) INFORMATION FOR SEQ ID NO: 927

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATTA	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
45 TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCCCTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCCGGAC	CGGATGCATT	CCCGATGGAC	350
CTGTCCTCAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
50 GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

2) INFORMATION FOR SEQ ID NO: 930

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 5 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

```

10 GCTATCTCTA AACAAAGCGGA AGCGGATATC GTGATTATCG CCGCCTGCGG      50
   TGAGCGTGCG AATGAGGTCTG TAGAGGTATT TACGGAGTTC CCGGAATTGG      100
   TAGACCCGCA TACGGGACGT AAATTGATGG AACGTACGAT CATTATCGCC      150
   AATACATCCA ACATGCCGGT AGCCGCTCGT GAGGCATCCG TATATACGGC      200
   GATGACCATC GCCGAGTATT ATCGCAGCAT GGGTTTGAAG GTTCTGTTGA      250
   TGGCCGACTC TACTTCCCGC TGGGCACAGG CTTTGCGTGA GATGTCCAAC      300
15 CGTTTGGAGG AGTTGCCGGG ACCGGATGCT TTCCCGATGG ACTTGTCGCG      350
   TATCGTGGCG AACTTCTACG CTCGTGCGGG ATTCGTTCAT TTGAATAACA      400
   ACGCTACAGG CTCCGTCACT TTCATCGGTA CGGTATCG      438

```

20

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

```

   CCTCCAGCAC GCTATCTCTA AGCAGGCGGA GGCTGATATC GTCATTATGG      50
   CAGCCTGCGG TGAGCGTGCT AATGAGGTGG TGGAGATCTT TGCCGAGTTC      100
   CCTGAGCTCG AAGACCCACA CACGGGACGC AAGCTGATGG AGCGTACGAT      150
40 CATCATCGCT AACACGAGTA ACATGCCAGT GGCTGCTCGT GAGGCTTCGG      200
   TCTACACCGC TATGACCATC GCTGAGTACT ACCGCTCGAT GGGTCTCAA      250
   GTACTCTTAA TGGCTGACTC GACCTCTCGC TGGGCACAGG CACTGCGTGA      300
   GATGTCTAAC CGTCTAGAGG AGCTGCCTGG ACCAGATGCA TTCCCGATGG      350
   ACTTGTCGGC TATCGTGGCA AACTTCTACG CTCGTGCCGG CTTCTGTCTAT      400
45 CTCAACAACG GTGAGACAGG TTCTGTAACC TTCATCGGTA CGGTCTCTCC      450
   AGC

```

50 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
 TTCATGAACA AATGTGACAT GGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA ATTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
 10 ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
 GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA 400
 CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
 15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTC CGTAAATTAC 500
 TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGT 550
 GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT 700
 20 TTCCGTAATA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
 AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
 CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

60 520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

2) INFORMATION FOR SEQ ID NO: 937

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATACIGARG YITTYGGIGA RTT

23

2) INFORMATION FOR SEQ ID NO: 938

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1203 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: D10023
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

```

ATGTCTCAAG TTCAAGAACA ACATATATCA GAGTCACAGC TTCAGTACGG      50
GAACGGTTCG TTGATGTCCA CTGTACCAGC AGACCTTTCA CAGTCAGTCG      100
TTGATGGAAA CGGCAACGGT AGCAGCGAAG ATATTGAGGC CACCAACGGC      150
20 TCCGGCGATG GTGGCGGATT GCAGGAGCAA GCGGAAGCGC AAGGTGAAAT      200
GGAGGATGAA GCATACGATG AAGCTGCCTT AGGTTCGTTT GTGCCAATAG      250
AAAAACTGCA AGTGAACGGG ATTACTATGG CGGATGTGAA AAAACTAAGG      300
GAGAGTGGGC TTCACACTGC TGAAGCGGTA TATCGGAAGC TAAGGCAGAT AAGTTGCTAA      350
TTTATTGGAA ATCAAAGGTA TATCGGAAGC TAAGGCAGAT AAGTTGCTAA      400
25 ACGAAGCGGC AAGGCTAGTG CCTATGGGAT TTGTCACGGC TGCTGATTTT      450
CATATGAGAA GATCGGAGCT GATTTGTTTG ACAACGGGTT CTAAGAATTT      500
GGACACTCTT TTGGGTGGTG GTGTGGAAAC TGGTTCTATT ACTGAGCTTT      550
TCGGTGAATT CAGGACAGGT AAGTCCCAGC TATGTCACAC TTTGGCCGTG      600
ACATGCCAAA TTCCATTGGA TATTGGTGGC GGTGAAGGTA AGTGTTTGTA      650
30 TATCGATACC GAAGGTACTT TCAGGCCCGT AAGATTGGTA TCCATAGCTC      700
AGCGGTTCGG ATTAGACCCG GATGATGCTT TGAACAACGT TCGGTATGCA      750
AGAGCCTATA ACGCCGATCA TCAGTTAAGA CTTCTGGATG CTGCTGCCCC      800
AATGATGAGC GAGTCTCGGT TTTCTTGAT TGTGGTCGAT TCTGTTATGG      850
CTCTATACCG TACGGATTTT TCTGGTCGTG GTGAACTAAG CGCAAGGCAA      900
35 ATGCATTTAG CCAAATTTAT GCGTGCTTTG CAAAGGCTGG CCGACCAATT      950
TGGTGTTCGA GTCGTCGTTA CTAACCAAGT GGTGCGCCAA GTTGATGGTG      1000
GTATGGCTTT TAATCCAGAT CCAAAGAAGC CTATCGGTGG TAATATTATG      1050
GCACATTCTT CCACCACGCG ATTAGGTTTC AAAAAGGGTA AGGGATGTCA      1100
AAGATTATGC AAAGTTGTTG ACTCACCTTG CTTACCAGAG GCTGAATGTG      1150
40 TGTTTCGCGAT CTATGAAGAT GGTGTTGGTG ACCCCAGAGA AGAAGACGAG      1200
TAG                                                                1203

```

45 2) INFORMATION FOR SEQ ID NO: 940

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: GRF88
 (C) ACCESSION NUMBER: M87549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA\	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAACCT	CTGCTGTAGA	GGTTCTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATAC	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
30	CAAAGCTAA	ATCAACATCT	TTTCAAAATG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptococcus humicolus*
 (B) STRAIN: ATCC 38294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

	CGTCCTTATC	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
	TCTCCGTCTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGACCTG	100
	TACCACGAGA	TGCGTGAGAC	TGGTGTTCATC	AACCTCGAGG	GCGACTCCAA	150
20	GGTCGCTCTC	GTCTTCGGCC	AGATGAACGA	GCCCCCGGA	GCCCGTGCCC	200
	GTGTCGCCCT	TACCGGCCTC	ACCATCGCCG	AGTACTTCCG	TGACGAGGAG	250
	GGTCAGGACG	TGCTTCTCTT	CATCGACAAC	ATTTTCCGTT	TCACCCAGGC	300
	CGGTTCCGAG	GTGTCTGCCC	TTCTCGGTCG	TATCCCCTCG	GCCGTCGGTT	350
	ACCAGCCCAC	CCTCGCTACC	GACATGGGTT	CCATGCAGGA	GCGTATCACC	400
25	ACCACCAAGA	AGGGTTTCGAT	TACCTCCGTC			430

2) INFORMATION FOR SEQ ID NO: 942

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

45	CGTGTACGAT	GCTCTTGAGG	TGCAAAAATGG	TAATGAGCGT	CTGGTGCTGG	50
	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TGCGTACCAT	CGCAATGGGT	100
	TCCTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAAGACC	TCGAACACCC	150
	GATCGAAGTC	CCGGTAGGTA	AAGCGACTCT	GGGCCGTATC	ATGAACGTAC	200
	TGGGTGAACC	GGTCGACATG	AAAGGCGAGA	TCGGTGAAGA	AGAGCGTTGG	250
50	GCGATTACAC	GCGCAGCACC	TTCTTACGAA	GAGCTGTCAA	ACTCTCAGGA	300
	ACTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	CCGTTTCGCTA	350
	AGGGCGGTAA	AGTTGGTCTG	TTCCGTTGGT	CGGGTGTAGG	TAAAACCGTA	400
	AACATGATGG	AGCTCATTCG	TAACATCGCG	ATCGAGCACT	CCGTTTACTC	450
	TGTGTTTTCG	GGCGTAGGTG	AACGTACTCG	TGAGGGGAAC	GACTTCTACC	500
55	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	GGTGTATGGC	550
	CAGATGAACG	AGCCGCCGGG	AAACCGTCTG	CGCGTAGCTC	TGACCGGTCT	600
	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTT	CTGCTGTTCG	650
	TTGACAACAT	CTATCGTTAC	ACCCTGGCCG	GTACGGAAGT	ATCCGCACTG	700
	CTGGGCCCGTA	TGCCTTCAGC	GGTAGGTTAT	CAGCCGACCC	TGGCGGAAGA	750
60	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAAACC	GGTT	794

2) INFORMATION FOR SEQ ID NO: 943

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG	50
	CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GCGGGCGGTA TCGTACGTAC	100
	CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG	150
	ACCTCGAACA CCCGATTGAA GTCCCAGTAG GTAAAGCGAC TCTGGGCCGT	200
	ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA	250
25	AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT	300
	CAAACCTCTCA GGAACCTGCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG	350
	TGTCCGTTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCGGGTGT	400
	AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC	450
	ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT	500
30	AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC	550
	CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG	600
	CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC	650
	GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG CCGGTACGGA	700
	AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA	750
35	CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAAA	800
	ACTGGTTCTA TCAC	814

40 2) INFORMATION FOR SEQ ID NO: 944

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55	GTGTACGATG CTCTTGAGGT GCAAAATGGT AATGAGCGTC TGGTGCTGGA	50
	AGTTCAGCAG CAGCTCGGCG GCGGTATCGT GCGTACCATC GCAATGGGTT	100
	CCTCCGACGG TCTGCGTCGC GGTCTGGATG TAAAGACCT CGAACACCCG	150
	ATCGAAGTCC CGGTAGGTAA AGCGACTCTG GGCCGTATCA TGAACGTACT	200
60	GGGTGAACCG GTCGACATGA AAGGCGAGAT CCGTGAAGAA GAGCGTTGGG	250

	CGATTCACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTIONAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTT	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTCGG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCgATCGAA	GTCCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTGATAAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

50

2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

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CGGACGCTAT CCCGCATGTT TACGATGCCC TGAAATTGGA CGAGAACGGT      50
CTGACTCTGG AAGTTCAACA ACTTCTGGGT GACGGCGTTG TCCGTACTAT      100
TGCAATGGGT AGTTCAGACG GCCTGAAACG CGGCATGTCT GTAAGCAATA      150
10 CTGGTGCGCC AATCACTGTG CCGGTAGGTA AAGGTACTTT GGGTCGTATT      200
GTCGACGTAT TGGGTACGCC TGTTGATGAA GCAGGTCCGA TCGATACCGA      250
CAAGAGCCGT GCCATTACCC AAACGTGCTCC GAAATTCGAC GAGTTGTCTG      300
CAACTACCGA ATTGTTGGAA ACCGGTATTA AAGTGATCGA CTTGCTGTGT      350
CCGTTTGCTA AAGGCGGTAA AGTAGGTCTG TTCGGTGGTG CCGGTGTAGG      400
15 CAAAACCGTG AACATGATGG AATTGATCAA CAACATCGCC AAAGCGCACA      450
GCGGTCTGTC CGTGTTTCGA GGTGTGGGCG AGCGTACCCG TGAAGGTAAC      500
GACTTCTACC ACGAGATGAA AGATTCCAAC GTATTGGATA AAGTGGCAAT      550
GGTTTACGGT CAGATGAACG AACCTCCGGG CAACCGTTTG CGCGTCGCAT      600
TGACCGGTTT GACCATGGCG GAATACTTCC GTGACGAAAA AGACGAAAAC      650
20 GGTAAGGTC GCGACGTATT GTTCTTCGTT GACAACATCT ACCGTTACAC      700
TCTGGCCGGT ACCGAAGTAT CTGCACTGTT GGGCCGTATG CTTTCTGCAG      750
TGGGTTACCA ACCGACATTG GCTGAAGAAA TGGGTCGTTT GCAAGAGCGT      800
ATTACCTCTA CCCAAACCGG TTCCATTACT TC                                832

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25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

```

TCCGCGCGAT GCCATTCCGC ATGTTTACGA CGCCCTGAAA TTGGATGCAA      50
ACGGCCTGAC TTTGGAAGTA CAACAGCTTC TGGGCGACGG CGTGGTTCGT      100
45 ACTATTGCAA TGGGTAGTTC GGACGGTCTG AAACGCGGCA TGAAGTAAG      150
CAATACAGAT GCGCCGATTA CTGTGCCGGT AGGTAAAGGT ACTTTGGGAC      200
GTATTGTCGA TGTGTTGGGT ACACCTGTTG ATGAAGCAGG TCCGATTGAT      250
ACCGACAAAC ACCGTGCTAT CCATCAGACA GCTCCGAAAT TCGATGAGTT      300
GTCTGCTACT ACCGAGCTGC TGGAAACAGG CATTAAAGTG ATTGACTTGC      350
50 TGTGTCCGTT TGCCAAAGGC GGTAAAGTAG GTCTGTTCGG TGGTGCCGGT      400
GTAGGCAAAA CCGTCAACAT GATGGAATTG ATTAACAACA TCGCCAAAGC      450
GCATAGTGTT TTGTCCGTGT TCGCCGGTGT GGGGGAACGT ACCCGTGAAG      500
GTAACGACTT CTACCACGAG ATGAAAGATT CCAACGTATT GGACAAAGTG      550
GCGATGGTTT ACGGTCAGAT GAACGAACCT CCGGGTAACC GTCTGCGTGT      600
55 AGCCTTGACC GGTTTGACGA TGGCCGAATA CTTCCGTGAT GAAAAAGACG      650
AAAGCGGCAA AGGTCGCGAC GTATTGTTCT TCGTGGACAA CATTTACCGT      700
TACACTCTGG CCGGTACAGA AGTATCCGCA TTGCTCGGTC GTATGCCTTC      750
AGCAGTAGGT TACCAACCGA CATTGGCTGA AGAAATGGGT CGTCTGCAAG      800
AGCGTATTAC CCTCTACTCA AACAGGCTCC ATTACTTCTA                        840

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60

2) INFORMATION FOR SEQ ID NO: 948

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

```

20 GCAGCTGGCG ACAAGCTACC TGAGATCAAT AATGCACTTG TAGTCTATAA      50
   AAATGACGAA AAAAAATCAA AAATCGTCCT TGAAGTAGCT CTTGAGCTTG      100
   GTGATGGAGT GGTTCCGACC ATCGCTATGG AATCAACGGA TGGGTTGACT      150
   CGTGGCATGG AAGTGCTAGA TACTGGCCGT CCAATTTCTG TGCCAGTCGG      200
   CAAAGAAACA CTTGGTCGCG TCTTTAACGT TTTGGGAGAT ACCATTGACT      250
   TGGATGCTCC TTTTGCGGAT GATGCAGAGC GCCAGCCAAT CCATAAGAAA      300
25 GCTCCAACCT TTGATGAGTT GTCTACTTCT TCAGAGATCT TAGAGACAGG      350
   TATCAAGGTT ATCGACCTGT TAGCCCCCTA TCTGAAAGGT GGTAAAGTTG      400
   GACTCTTCGG TGGTGCCGGA GTTGGTAAGA CCGTCCTGAT TCAAGAATTG      450
   ATCCACAACA TTGCCAAGA ACACGGTGGT ATTTCTGTAT TTAGTGGCGT      500
   TGGGGAACGT ACCCGTGAAG GGAATGACCT TTATTGGGAA ATGAAAGAGT      550
30 CTGGTGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAGAT GAATGAGCCG      600
   CCAGGAGCGC GTATGCGGGT TGCTTTGACT GGTTTGACGA TTGCAGAATA      650
   CTTCCGTGAT GTGGAAGGTC AAGATGTCTT GCTCTTCATT GACAACATCT      700
   TCCGTTTCAC GCAGGCAGGT TCTGAAGTTT CTGCCCTTTT GGGTCGGATG      750
   CCGTCAGCCG TTGGTTACCA ACCAACACTT GCGACAGAAA TGGGGCAATT      800
35 GCAAGAGCGT ATCACATCGA CTAAGAAGGG TTCTGTAACC TCT              843

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2) INFORMATION FOR SEQ ID NO: 949

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

```

55 GCAGCAGGGG AAAAAGTTCC TGAGATTAAC AATGCACTTG TCGTCTACAA      50
   AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTGG      100
   GAGATGGTAT GGTCCGTACT ATCGCCATGG AATCAACAGA TGGTTTACTG      150
   CGTGGAATGG AAGTATTGGA CACAGGTCGT CCAATCTCTG TACCAGTAGG      200
   TAAAGAAACT TTGGGACGTG TCTTCAATGT TTTGGGAGAT ACCATTGACT      250
60 TGGAAGCTCC TTTTACAGAA GATGCAGAGC GTCAGCCAAT TCATAAAAAA      300

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	GCTCCAACCTT	TTGATGAATT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAGGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTTCAGTAT	TTACCGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GTAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGTGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTAACT	GGTTTGACAA	TCGCCGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAGCGT	ATTACATCAA	CTAAAAAGGG	TTCTGTAACC	T	841

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTGTAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	GTAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT	150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAAA	GAAACACTTG	200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT	250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA	300
	TGAGTTGTCT	ACTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG	350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT	400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTGAG	GAATTGATCC	ACAACATTCG	450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC	500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG	550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT	600
	GCGGGTTGCT	TTGACTGGTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG	650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG	700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG	750
	TTACCAACCA	ACACTTGCGA	CTGAAATGGG	ACAACCTCAA	GAGCGTATTA	800
	CATCGACTAA	GAAAGGTTCT	GTAACCTT			827

50

2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus oralis*

(B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

	GCAGCAGGGG	AAACACTTCC	TGAGATTAAT	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GTGATGGTAT	GGTCCGTACG	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
10	CGTGGAATGG	AAGTTTGGGA	CACAGGCCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACTATTGACT	250
	TGGATGCTCC	TTTCGCTGAA	GACGCTGAGC	GTCAGCCAAT	TCATAAGAAA	300
	GCTCCAACCT	TTGATGAATT	GTCTACCTCA	TCTGAAATCT	TGGAAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGGAAAGTTG	400
15	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTGAT	CCAAGAGTTG	450
	ATTCACAACA	TTGCCCAAGA	ACATGGTGGT	ATTTCAAGTAT	TTACCGGTGT	500
	TGGAGAACGT	ACCCGTGAGG	GGAACGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCA	600
	CCTGGAGCAC	GTATGCGTGT	TGCTCTTACT	GGTTTGACAA	TCGCCGAATA	650
20	CTTCCGTGAT	GTAGAAGGCC	AAGATGTGCT	TCTCTTTATC	GACAAATATCT	700
	TCCGTTTCAC	TCAAGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTTCGGATG	750
	CCTTCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CTAAGAAGGG	TTCTGTAACC	TCTA	844

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
45	GAGATGGTAT	GGTTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	250
	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300
	GCTCCAACCT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
50	GATCAAGGTT	ATTGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTCAAGTAT	TTACTGGTGT	500
	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
55	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTTCGTATG	750
	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG			830

60

2) INFORMATION FOR SEQ ID NO: 953

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
20	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACTT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAACTT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATCAAGGTT	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTGCTGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA	844

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACTT	300
	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA		834

50

2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microti*
 (B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGGTTCACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTAA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTTACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTTCAGGAC	GTCTTGACAG	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGACGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

2) INFORMATION FOR SEQ ID NO: 958

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

```

5  TACAACACCA ACTTGCTAAA TGGGCAGATG CAGAAGTAGT TGTTTATGTT      50
   GGTGTGTTGGG AACGTGGAAA TGAAATGACC GATGTACTTA TGGAATTCCC      100
   AGAAATTATT GACCCTAAGA CAGGACAATC TTTAATGAAG AGAACAGTTC      150
   TTATAGCTAA TACTTCTAAT ATGCCAGTTG CTGCTCGTGA GGCTTCAATC      200
   TATACTGGTA TAACTATTGC AGAATATTTT AGAGATATGG GATATTCAGT      250
10  GGCACCTTATG GCAGATTCAA CAAGTCGTTG GGCAGAAGCA CTTTCGTGAAA      300
   TGTCAGGACG TTTGGAAGAA ATGCCAGGTG ATGAAGGATA TCCAGCATAT      350
   CTATCAAGTA GAATAGCAGA GTTTTATGAA AGAGCAGGGC TTGTTGAATG      400
   TCTAGGTAAT GGAGAAGAAG GAGCATTAACTGTAATTGGA GCAGTATCTC      450
   CA                                                                452

```

15

2) INFORMATION FOR SEQ ID NO: 959

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

```

TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TGCGTCATCT      50
35  ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100
   TTCCCGACCC TGACGACCGT GATCAATGGT CGCGAGGAGT CGATCATGAA      150
   GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
   AGGCCTCTAT TTACACCGGC ATCACCTTGG CCGAGTACTA CCGTGATATG      250
   GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
40  GCTTCGTGAG ATTTCTGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
   ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CTTTCTACGA GCGCGCCGGC      400
   CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
   CCGTGCCCGT TCTCCGCCG                                                                469

```

45

2) INFORMATION FOR SEQ ID NO: 960

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

```

      TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT      50
      ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100
5     TTCCCGACCC TGACGACCGT GATCGATGGT CGCGAGGAGT CGATCATGAA      150
      GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
      AGGCCTCTAT TTACACCGGC ATCACCCTGG CCGAGTACTA CCGTGATATG      250
      GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
      GCTTCGTGAG ATTTCCGGGTC GTTTGGCGGA GATGCCGGCC GATGGTGGCT      350
10    ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CTTTCTACGA GCGCGCCGGC      400
      CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
      CCGTGCCGTG TCTCCGCCG                                     469

```

15

2) INFORMATION FOR SEQ ID NO: 961

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania guyanensis*
 - (B) STRAIN: ATCC 50126

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

```

      TGTATCAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TGTGTCATCT      50
      ATGTCGGCTG CGGTGAACGC GGTAACGAGA TGGCCGAGGT GCTCATGGAG      100
      TTCCCGACCC TGACGACTGT GATCGATGGT CGCGAAGAGT CCATCATGAA      150
35    GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCCGTC GCAGCCCGTG      200
      AGGCCTCTAT TTATACCGGC ATCACCCTTG CTGAGTACTA CCGTGATATG      250
      GGCAAGCACA TTGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
      GCTGCGTGAG ATTTCCGGGTC GATTGGCGGA GATGCCGGCT GATGGTGGCT      350
      ACCCTGCCTA CCTCAGCGCC CGCCTCGCCT CTTTCTACGA GCGCGCCGGT      400
40    CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT      450
      CCGTGCACTG TCTCCACCG                                     469

```

45 2) INFORMATION FOR SEQ ID NO: 962

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania donovani*
 - (B) STRAIN: ATCC 50212

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCCACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCAGTC	GCAGCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCCGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Leishmania hertigi*
- (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TTCCCCACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCCAA	CATGCCAGTT	GCAGCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCACACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCCGGTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
40	TGGTGCGGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 964

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Leishmania mexicana*
- (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

	TTCCCCGACCC	TGACGACCAT	GATCGATGGT	CGGGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCCCGTC	GCAGCCCCGTG	200
	AGGCCTCTAT	CTACACCGGC	ATCACCTCG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCTGAGGC	300
5	GCTTCGTGAG	ATTTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCCGTG	TCTCCGCCG				469

10

2) INFORMATION FOR SEQ ID NO: 965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
30	TTCCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
35	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

40

2) INFORMATION FOR SEQ ID NO: 966

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 449 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

	CACCAGTTCG	CCAAGTGGGC	AGATGCTCAG	ATAGTTGTAT	ACGTTGGTTG	50
	TGGAGAACGT	GGTAACGAGA	TGACAGACGT	TCTAAATGAA	TTCCCAGAAC	100
	TGATTGACCC	TCATACAGGC	GAATCTCTAA	TGAAGAGAAC	AGTTCTTATA	150
60	GCTAATACGT	CAAATATGCC	AGTTGCAGCC	AGAGAGGCAA	GTATATATAC	200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCCACC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGAG	CGGCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCTTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTT	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCT	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCGG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCGTG	GCACGGTGTT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGTACATT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

	CGATCCTGGT	GGTGTGCGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTTCCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCG	CGAACTGCTG	AGCAAGTACG	ATTTCCCGGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTG	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGGTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCACG	GTGGTGACTG	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAGAC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATGCCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTACTGTTGC	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTCG	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTTGAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCACATG	TGAAGTGTAC	600
	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

50

2) INFORMATION FOR SEQ ID NO: 970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 5 (B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

```

10 TATGCCTCAA ACACGTGAAC ACATCTTGTT ATCACGTAAC GTTGGTGTAC      50
   CATACATCGT TGTTTTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA      100
   TTACTAGAAT TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATATGA      150
   CTTCCCAGGC GACGATGTTT CTGTAATCGC TGGTTCTGCT TTGAAAGCTC      200
   TTGAAGGCGA TGCTTCATAC GAAGAAAAAA TCATGGAATT AATGGCTGCA      250
   GTTGACGAAT ACGTTCCAAC TCCAGAACGT GACACTGACA AACCATTTCAT      300
15 GATGCCAGTC GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA      350
   CAGGCCGTGT TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC      400
   GTTGGTATTG CTGAAGAAAC TGCTAAAACA ACTGTAAGTGT GTGTTGAAAT      450
   GTTCCGTAAA TTGTTAGACT ATGCTGAAGC AGGGGATAAC ATTGGTGCAAT      500
   TGCTACGTGG GGTGCTCGT GAAGACATCC AACGTGGACA AGTATTAGCT      550
20 AAAGCTGGTA CAATCACACC TCATACAAAA TTAAAGCTG AAGTTTACGT      600
   TTTAACAAAA GAAGAAGGTG GACGTCACAC TCCA                      634

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25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 35 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

```

40 GGACCAATGC CACAACTCG TGAGCACATC CTTCTTTCAC GTCAGGTTGG      50
   TGTTAAACAC CTTATCGTCT TCATGAACAA AGTTGACTTG GTTGACGACG      100
   AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT ATTGTCAGAA      150
   TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA      200
45 AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA      250
   ACACAGTTGA TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA      300
   TTGCTTCTTC CAGTCGAGGA CGTATTCTCA ATCACTGGAC GTGGTACAGT      350
   TGCTTCAGGA CGTATCGACC GTGGTATCGT TAAAGTCAAC GACGAAATCG      400
   AAATCGTTGG TATCAAAGAA GAAACTCAAA AAGCAGTTGT TACTGGTGTG      450
50 GAAATGTTCC GTAAACAAC TGAACGAAGG CTTGCTGGAG ATAACGTAGG      500
   TGTCCTTCTT CGTGGTGTTC AACGTGATGA AATCGAACGT GGACAAGTTA      550
   TCGCTAAACC AGGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTC      600
   TACATCCTTA CTAAAGAAGA AGGTGGACGT CACACTCCAT TCTTCAACAA      650
   CTACCGTCCA CAATTCTACT TCCGTACTAC TGACGTTACA GGTTCATTCG      700
55 AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA CGTGACAATC      750
   GACGTTGAGT TGATTCACCC AATCGCCGTA GAACAAG                      787

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60 2) INFORMATION FOR SEQ ID NO: 972

540

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

15 TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA GCACATCCTG 50
 CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC TGAACAAATG 100
 CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA ATGGAAGTTC 150
 GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC TCCGATCGTT 200
 20 CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT GGGAAGCGAA 250
 AATCCTGGAA CTGGCTGGCT TCCTGGATTC TTACATTCCG GAACCAGAGC 300
 GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT ATTCTCCATC 350
 TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG GTATCATCAA 400
 AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT CAGAAGTCTA 450
 25 CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA AGGCCGTGCT 500
 GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG AAGAAATCGA 550
 ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG CACACCAAGT 600
 TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG CCGTCATACT 650
 CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA CTACTGACGT 700
 30 GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA ATGCCGGGCG 750
 ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC GATGGACGAC 800
 GGT 803

35 2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

ACTGACGGCC CGATGCCGCA GACTCGTGAG CACATCCTGC TGGGTCGTCA 50
 GGTAGGCGTT CCGTACATCA TCGTGTTCCCT GAACAAATGC GACATGGTTG 100
 ATGACGAAGA GCTGCTGGAA CTGGTTGAAA TGGAAGTTCG TGAACCTCTG 150
 55 TCTCAGTACG ACTTCCCGGG CGACGACACT CCGATCGTTC GTGGTTCTGC 200
 TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG GGAAGCGAAA ATCCTGGAAC 250
 TGGCTGGCTT CCTGGATTCC TACATTCCGG AACCAGAGCG TGCRATTGAC 300
 AAGCCGTTCC TGCTGCCGAT CGAAGACGTA TTCTCCATCT CCGGTCGTGG 350
 TACCGTTGTT ACCGGTCGTG TAGAACGCGG TATCATCAAA GTTGGTGAAG 400
 60 AAGTTGAAAT CGTTGGTATC AAAGAGACTC AGAAGTCTAC CTGTACTGGC 450

	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	GGCCGTGCTG	GTGAGAACGT	500
	AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	AGAAATCGAA	CGTGGTCAGG	550
	TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	ACACCAAGTT	CGAATCTGAA	600
	GTGTACATTC	TGTCCAAAGA	TGAAGGCGGC	CGTCATACTC	CGTTCTTCAA	650
5	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	TACTGACGTG	ACTGGTACCA	700
	TTGAACTGCC	GGAAGGCGTA	GAGATGGTAA	TGCCGGGCGA	CAACATCAAA	750
	ATGGTTGTTA	CC				762

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2) INFORMATION FOR SEQ ID NO: 974

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 804 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 11775

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
30	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCAGGCGAC	GACACTCCGA	200
	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCCTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
35	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GCGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGTCGTC	650
40	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGA					804

45

2) INFORMATION FOR SEQ ID NO: 975

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 804 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

```

5   GCGATCCTGG TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA      50
   GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC      100
   TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA      150
   ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GACTTCCCCG GCGACGACAC      200
   TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT      250
   GGGAAGCGAA AATCCTGGAA CTGGCTGGCT TCCTGGATTC YTACATTCCG      300
   GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT      350
10  ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG      400
   GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT      450
   CAGAAGTCTA CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
   AGGCCGTGCT GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG      550
   AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG      600
15  CACACCAAGT TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG      650
   TCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA      700
   CTACTGACGT GACTGGTACC ATCGAACTGC CGGAAGGTGT AGAGATGGTA      750
   ATGCCGGGCG ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC      800
   GATG                                     804
20

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2) INFORMATION FOR SEQ ID NO: 976

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25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 825 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Mycobacterium avium
          (B) STRAIN: Mavi-1
35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

```

40  GGCGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCCGATGC CGCAGACCCG      50
   TGAGCACGTG CTGCTCGCCC GTCAGGTCGG TGTGCCCTAC ATCCTGGTCG      100
   CCCTGAACAA GGCCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC      150
   GAGATGGAGG TCCGCGAGCT GCTGGCCGCC CAGGAGTTCG ACGAGGACGC      200
   CCCGGTGGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGC GACGCCAAGT      250
   GGGTCGAGTC CGTCGAGCAG CTGATGGAGG CCGTCGACGA GTCGATCCCG      300
45  GACCCGGTCC GCGAGACGGA GAAGCCGTTT CTGATGCCGG TGGAGGACGT      350
   CTTACCATC ACCGGGCGTG GCACCGTGGT CACCGGTCGT GTCGAGCGCG      400
   GTGTGATCAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CCGCCCACC      450
   AGCACCAAGA CCACGGTCAC CGGTGTGGAR ATGTTCCGCA AGCTGCTCGA      500
   CCAGGGCCAG GCCGGTGACA ACGTCGGTCT GCTGCTGCGT GGTATCAAGC      550
50  GTGAGGACGT CGAGCGCGGC CAGGTCGTGA CCAAGCCCGG CACCACCACG      600
   CCGCACACCG AGTTCGAGGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
   CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC      700
   GCACCACCGA CGTGACCGGT GTGGTGACGC TGCCGGAGGG CACCGAGATG      750
   GTGATGCCCC GTGACAACAC CAACATCTCG GTGAAGCTGA TCCAGCCCGT      800
55  CGCCATGGAC GACGGTSTGC GGTTC                                     825

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2) INFORMATION FOR SEQ ID NO: 977

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

```

15  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
    AACAAAGTTG ACTTGGTTGA CGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTATTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTTACAGCA CTTAAAGCTC TTGAAGGTGA CTCTAAATAC      250
20  GAAGACATCG TTATGGAATT GATGAACACA GTTGATGAGT ATATCCCAGA      300
    ACCAGAACGT GACACTGACA AACCATTGCT TCTTCCAGTC GAGGACGTAT      350
    TCTCAATCAC TGGACGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ATCGTTAAAG TCAACGACGA AATCGAAATT GTTGGTATCA AAGAAGAAAC      450
    TCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAACTTGACG      500
25  AAGGTCTTGC TGGAGATAAC GTAGGTGTCC TTCTTCGTGG TGTTCAACGT      550
    GATGAAATCG AACGTGGACA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAAGGTG AAGTCTACAT CCTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAAC TACC GTCCACAATT CTACTTCCGT      700
    ACTACTGACG TTACAGGTTC AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
30  AATGCCTGGT GATAACGTGA CAATCGACGT TGAGTTGATT CACCCAATCG      800
    CCGTAGAACA AGGTACTACA                                820
  
```

35 2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

```

50  GGCGCGATCC TGGTGGTCGC CGCCACCGAT GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTGGG CGTGCCCTAC ATCCTGGTGG      100
    CGCTGAACAA GTCCGACGCG GTCGACGACG AGGAGCTGCT CGAGCTCGTC      150
    GAGCTGGAGG TCCGCGAGTT GCTGGCCGCC CAGGACTTCG ACGAGGAAGC      200
55  TCCGGTGGTC CGGGTCTCGG CGCTGAAGGC GCTCGAGGGC GACGCCACCT      250
    GGGTGAAGTC GGTAGAGGAC TTGATGGACG CGGTGACGCA GTCGATTCCG      300
    GACCCGGTCC GCGACACCGA CAAGCCGTTT CTGATGCCCC TCGAGGACGT      350
    CTTACCATC ACCGGTCGTG GCACCGTCGT CACCGGCCGT GTGGAGCGCG      400
    GCGTGGTGAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CAAGCCGACC      450
60  AGCACCAAGA CCACGGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
  
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	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCGG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCGT	800
	CGCCATGGAC	GACGGTCTGC	GG			822

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2) INFORMATION FOR SEQ ID NO: 979

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-11

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTG GTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTT CAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTG TAAA	TGTTCCGTAA	ACAACTTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAAC TAC	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	CCCGTAGAAC	AAGGTACTAC	A			821

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2) INFORMATION FOR SEQ ID NO: 980

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: ATCC 25177

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
5	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCGG	TCGAGGACGT	350
10	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTGCGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550
	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600
15	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
20	CGCCATGGAC	GAAGGTNTGC	GTTTCGCG			828

2) INFORMATION FOR SEQ ID NO: 981

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 144

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGCCCAATG	CCACAAACTC	50
40	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
45	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTT	550
50	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTAATA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTAATCGCTC	800
55	CAATCGCGAT	TGAAGACGG				819

2) INFORMATION FOR SEQ ID NO: 982

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

```

15  CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
    CACATCCTTC TTTCACGTCA GGTTGGTGTT AAACACCTTA TCGTCTTCAT      100
    GAACAAGATC GACTTGGTTG ATGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
    TGGAAATCCG TGACCTCTTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
    CCAGTTATCC AAGGTTTCAGC TCTTAAAGCT CTTGAAGGTG ATACTAAGTA      250
20  CGAAGACATC ATCATGGAAT TGATGAACAC TGTTGATGAG TACATCCCAG      300
    AACCAGAACG TGATACTGAC AAACCTCTTC TTCTTCCAGT CGAAGACGTA      350
    TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
    TACTGTTCGT GTCAACGATG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
    TCCAAAAGC  AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAGCTTGAC      500
25  GAAGGTCTTG CAGGGGACAA CGTAGGTGTA CTTCTTCGTG GTATCCAACG      550
    TGATGAAATC GAACGTGGTC AAGTTATCGC TAAACCAGGT TCAATCAACC      600
    CACACACTAA ATTCAGGGT  GAAGTTTACA TCCTTACTAA AGAAGAAGGT      650
    GGACGTCACA CTCCATTCTT CAACAAC TACGTCACAGT TCTACTTCCG      700
    TACAAC TGACGTTTCAAGGTT CAATCGAACT TCCAGCAGGT ACTGAAATGG      750
30  TAATGCCTGG TGATAACGTA ACTATCGACG TTGAGTTGAT CCACCCAATC      800
    GCCGTTGAAC AAGG                                     814
  
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35 2) INFORMATION FOR SEQ ID NO: 983

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

```

50  CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
    CACATCCTTC TTTCACGTCA GGTTGGTGTT AAACACCTTA TCGTCTTCAT      100
    GAACAAAGTT GACTTGGTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
    TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
55  CCAGTTATCC AAGGTTTCAGC TCTTAAAGCC CTTGAAGGTG AACTAAATA      250
    CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG      300
    AACCAGAACG TGACACTGAC AAACCATTCG TTCTTCCAGT CGAAGACGTA      350
    TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
    TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
60  CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC      500
  
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	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	CCCGTAGAAC					810

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2) INFORMATION FOR SEQ ID NO: 984

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTA	AGCTTCA	ACTGAC	GACGGAC	CAA	TGCCACA	AAAC	TCGTGAG	CAC	50
	ATCCTTCT	TTT	CACGTC	AGGT	TGGTGTT	AAA	CACCTT	TATCG	TCTTCAT	GAA
	CAAGATCG	AC	TTGGTT	GATG	ACGAAGA	ATT	GCTTGA	ATTG	GTTGAA	ATGG
30	AAATCCGT	GGA	CCTCTT	GTCA	GAATAC	GACT	TCCCAG	GTTGA	CGATCT	TCCA
	GTTATCCA	AG	GTTCA	GCTCT	TAAAGCT	CTT	GAAGGT	GATA	CTAAGT	ACGA
	AGACATCA	TATC	ATGGA	ATTGA	TGAACAC	TGT	TGATGA	GATAC	ATCCCAG	AAC
	CAGAACGT	GGA	TACTGA	CAAA	CCTCTT	CTTC	TTCCAG	TCTGA	AGACGT	ATTC
	TCAATCA	CTG	GTCGT	GGTAC	AGTTG	CTTCA	GGACGT	TATCG	ACCGTG	GTTAC
35	TGTTTCGT	GTG	AACGAT	GAAA	TCGAA	ATCGT	TGGTAT	CAAA	GAAGAA	ATCC
	AAAAAGCA	GT	TGTTACT	GGT	GTTGAA	ATGT	TCCGTA	AAACA	GCTTGAC	GAA
	GGTCTTG	CAG	GGGACA	ACGT	AGGTGT	ACTT	CTTCGT	GTTA	TCCAAC	GTTGA
	TGAAATCG	AA	CGTGGT	CAAG	TTATCG	CTAA	ACCAGG	TTCA	ATCAACC	CAC
	ACACTAA	ATT	CAAGGG	TGAA	GTTTAC	ATCC	TTACTA	AAAGA	AGAAGG	TGGA
40	CGTCACAC	TC	CATTCT	TCAA	CAACTAC	CGT	CCACAG	TTCT	ACTTCC	GTTAC
	AACTGAC	GTT	ACAGGT	TCAA	TCGAA	CTTCC	AGCAGG	TACT	GAAATG	GTTAA
	TGCCTGG	TGA	TAACGT	AACT	ATCGAC	GTTG	AGTTGA	TCCA	CCCAAT	CGCC
	GTTGAACA	AG	GTACTAC							817

45

2) INFORMATION FOR SEQ ID NO: 985

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTTAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTC	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	GTTTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCTGA	AGACGTATTG	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTTCGTGTC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACTTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

20

2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAACTCG	TGAGCACATC	50
	CTTCTTTTAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

55

2) INFORMATION FOR SEQ ID NO: 987

(i) SEQUENCE CHARACTERISTICS:

549

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
15	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAA	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTCGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTT	CGTAAACGCT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTAGTATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCCTGTTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TGAAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTC	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTAAGTAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45

2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

	GGATCCTGTA	TATGCACAAA	AACTAGGTGT	TAACATCGAT	GAATTACTAT	50
	TATCACAACC	TGATACAGGG	GAGCAAGGTT	TAGAAATCGC	AGAAGCACTT	100
	GTACGAAGTG	GTGCGGTTGA	TATTATCGTA	ATTGACTCTG	TAGCAGCTCT	150
5	TGTA					154

2) INFORMATION FOR SEQ ID NO: 991

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25	GCCATTGCAG	AGGCACAGAA	GCAGGGCGGT	ATTGCAGCCT	TCATTGATGC	50
	TGAGCACGCC	TTCGACCGTT	TCTATGCAGA	GAAGTTAGGT	GTGGATGTTG	100
	ATAACCTTTG	GGTTTCACAG	CCAGACAATG	GTGAGCAGGC	TTTAGAGATT	150
	GCCGACCAGC	TGATTCGCTC	TTCCGCTATT	GACATTCTCG	TTGTCGACTC	200
	AGTTGCAGCC	TTGACTCCAA	AGAAGGAGAT	TGAGGGTGAC	ATGGGTGACT	250
30	CTGCAGTAGG	TTTACAAGCA	CGACTGATGA	GTCAGGCATT	GCGTAAACTT	300
	ACCTCAACAA	TCGCAAAAAC	TAATACTTGC	TGCATCTTCA	TCAACCAGTT	350
	GCGTGAGAA	ATTGGTGTGA	TGTTTGGTAA	TCCA		384

35

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	CATACATCGT	50
	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	TTACTAGAAT	100
	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAAATATGA	CTTCCCAGGC	150
55	GACGATGTT	CTGTAATCGC	TGGTTCGCT	TTGAAAGCTC	TTGAAGGCGA	200
	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	GTTGACGAAT	250
	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTCAT	GATGCCAGTC	300
	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	CAGGCCGTGT	350
	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	GTTGGTATTG	400
60	CTGAAGAAAC	TGCTAAAACA	ACTGTAAC	GTGTTGAAAT	GTTCCGTAAA	450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (C) ACCESSION NUMBER: extracted from U40453

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTTAGT	50
GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAAC TTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCTGTT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAACCTAAGA	ACCAAGAGAT	GGCAACTTTA	300
TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTTAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
35 CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACAACC	750
AAGTAA					756

40

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995
10 ACATTCTCGT GAGTAACAGG GT 22

15 2) INFORMATION FOR SEQ ID NO: 996

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996
 ACAAATCATG AAGGGAATCA TTTAG 25

30 2) INFORMATION FOR SEQ ID NO: 997

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997
 CTAATTCTTG AGCAGTTACC ATT 23

45 2) INFORMATION FOR SEQ ID NO: 998

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998
 GGAGGGGTAA CAAATCATGA AGG 23

60

2) INFORMATION FOR SEQ ID NO: 999

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999

15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000

30 TTAGTGTGTG GGTGATTGA ACT

23

35 2) INFORMATION FOR SEQ ID NO: 1001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001

AAGAGTTGCT TGAATTAGTT GAG

23

50 2) INFORMATION FOR SEQ ID NO: 1002

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

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AACATGATCA CTGGTGCCGC TCAAAATGGAC GGAGCTATCC TTGTAGTTGC      50
TTCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC CTTCTTTCAC      100
GTCAGGTTGG TGTTAAACAC CTTATCGTGT TCATGAACAA AGTTGACCTT      150
10 GTTGATGACG AAGAGTTGCT TGAATTAGTT GAGATGGAAA TTCGTGACCT      200
TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT ATCCAAGGTT      250
CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG      300
GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC      350
TGACAAACCA TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC      400
15 GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTACTGT TCGTGTC AAC      450
GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTAAAA AAGCTGTTGT      500
TACTGGTGTT GAAATGTTCC GTAAACAAC TACGGAAGGT CTTGCAGGAG      550
ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT      600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCACACCA CTAAATTCAA      650
20 AGGTGAAGTA TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT      700
TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACAAC TGACGTAACA      750
GGTTCAATCG AACTTCCAGC AGGTACAGAA ATGGTTATGC CTGGTGATAA      800
CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA GAACAAGGTA      850
CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT          894
25

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2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 40 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

```

AATGGATCCT GTATATGCAC AAAAAATTAGG CGTTAACATA GATGAATTAC      50
45 TATTATCACA GCCTGATACA GGGGAGCAAG GATTAGAAAT CGCGGAAGCA      100
CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC      150
TCTTGTACCG AAAGCAGAGA TTGAAGGCCA CATGGGTGAC TCACACGTAG      200
GTTTACAAGC ACGTTTAATG TCACAAGCAC TTCGTAAGCT TTCAGGAGCA      250
ATCAACAAAT CAAAAACAAT TGCAATCTTT ATTAACCAA TTCGTGAAAA      300
50 AGTTGGGGTT ATGTTCTGGAA ACCCAGAAAC AA          332

```

2) INFORMATION FOR SEQ ID NO: 1004

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

```

10 ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAACTC CGATCAATAC      50
   GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
   TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
   ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGACTGGGGT      200
   TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
15 TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
   GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT      350
   ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
   TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
   GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA      500
20 ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550
   TTATGCTGCC TTTGCAAATG GTGGCACTTA CTATAAACCA ATGTATATCC      600
   ATAAAGTCGT CTTCAGTGAT GGAAGTAAAA AAGAGTTCTC TAATGTCGGA      650
   ACTCGTGCCA TGAAGGAAAC GACAGCCTAT ATGATGACCG ACATGATGAA      700
   AACAGTCTTG ACTTATGGAA CTGGGCGTGG AGCCTATCTT CCTTGGCTTC      750
25 CTCAAGCTGG TAAACACAGG ACCTCTAACT ATACAGATGA GGAAGTTGAA      800
   AACCACATCA AGAACACTGG CTATGTAGCT CCAGATGAAA TGTTTGTTGG      850
   TTATACTCGT AAGTATTCTA TGGCTGTATG GACAGGTTAT TCGAATCGTT      900
   TAACTCCTAT CGTTGGAGAT GGTTCCTAG TTGCAGCTAA AGTTTATCGC      950
   TCCATGATAA CGTATCTATC AGAAGATACT CATCCAGAAG ACTGGACGAT     1000
30 GCCAGACGGA CTTTTCAGAA ACGGGGAATT TGTATTCAAA AATGGAGCTC     1050
   GCCCAATATG GACTGAACCC TCTACTCAAC AATCCTCAAC AGCTGAAAGT     1100
   TCAAGCTCAT CATCAGATAG TTCAACTTCA CAGTCTAGCT CAACCACTCC     1150
   AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT     1200
   CAAATACAAC CC                                           1212
35

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2) INFORMATION FOR SEQ ID NO: 1005

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

```

55 AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA ATACGTCTCT      50
   TACCTTGACG ATGATTTGCA AGTCGCATCT ACGGTCGTAG ATGTTTCAAA     100
   TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA AGTAACGTTT     150
   CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG GGGTTCTGCT     200
   ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG GTGTTTATGA     250
   TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT CCGGAACAA      300
60 GCACACCTGT CTACAACTGG GATAGAGCAT ATTTCCGTAA TATTACTCTG      350

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	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAA	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACATG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGCCATAC	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
55	TTTACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAACCTC CGATCAATAC 50
GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT 100
TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA 150
25 ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGACTGGGGT 200
TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT 250
TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG 300
GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT 350
ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC 400
30 TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG 450
GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA 500
ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC 550
TTATGCTGCC TTTGCAAATG GTGGCACTTA CTATAAACCA ATGTATATCC 600
ATAAAGTCGT CTTCAGTGAT GGAAGTAAAA AAGAGTTCTC TAATGTCGGA 650
35 ACTCGTGCCA TGAAGGAAAC GACAGCCTAT ATGATGACCG ACATGATGAA 700
AACAGTCTTG ACTTATGGAA CTGGGCGTGG AGCCTATCTT CCTTGGCTTC 750
CTCAAGCTGG TAAACAGGA ACCTCTAACT ATACAGATGA GGAAGTTGAA 800
AACCACATCA AGAACACTGG CTATGTAGCT CCAGATGAAA TGTTTGTG 850
TTATACTCGT AAGTATTCTA TGGCTGTATG GACAGGTTAT TCGAATCGTT 900
40 TAATCCTAT CGTTGGAGAT GGTTCCTAG TTGCAGCTAA AGTTTATCGC 950
TCAATGATAA CGTATCTATC AGAAGATACT CATCCAGAAG ACTGGACGAT 1000
GCCAGACGGA CTTTTAGAA ACGGGGAATT TGTATTCAAA AATGGAGCTC 1050
GCCCAATATG GACTGAACCC TCTACTCAAC AATCCTCAAC AGCTGAAAGT 1100
TCAAGCTCAT CATCAGATAG TTCAACTTCA CAGTCTAGCT CAACCACTCC 1150
45 AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCCTGATC 1218

50 2) INFORMATION FOR SEQ ID NO: 1008

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

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5  GTAGACCAAG AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA      50
   ATACGTCTCT TACCCTGACG ATGATTTGCA AGTCGCATCT ACGGTCGTAG      100
   ATGTTTCAAA TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA      150
   AGTAACGTTT CATTGTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG      200
10  GGGTTCTGCT ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG      250
   GTGTTTATGA TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT      300
   CCGGGAACAA GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTTCGGTAA      350
   TATTACTCTG CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG      400
   AGACTTTGAA TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT      450
15  CTTGGTATCG ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA      500
   TACAACAGAA TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG      550
   CTGCTTATGC TGCCTTTGCA AATGGTGGCA CTTACTATAA ACCAATGTAT      600
   ATCCATAAAG TCGTCTTCAG TAATGGAAGT AAAAAAGAGT TCTCTAATGT      650
   CGGAACCTCG GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA      700
20  TGAAAACAGT CTTGACTTAT GGAAGTGGGC GTGGAGCCTA TCTTCCTTGG      750
   CTTCTCTAAG CTGGTAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT      800
   TGAAAACCAC ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG      850
   TTGGTTATAC TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCGAAT      900
   CGTTTAACTC CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA      950
25  TCGCTCAATG ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA     1000
   CGATGCCAGA CGGACTTTTC AGAAACGGGG AATTTGTATT CAAAAATGGA     1050
   GCTCGCCCAA TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA     1100
   AAGTTCAAGC TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA     1150
   CTCCAAGCAC AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA     1200
30  CAATCAAATA CAACCCCTGA TCA                                     1223

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2) INFORMATION FOR SEQ ID NO: 1009

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35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1214 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
40  (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
45  (A) ORGANISM: Streptococcus pneumoniae
      (B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

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50  ACCAAGAAGC TCAAAAACAT CTGTGGGGATA TCTACAACTC CGATCAATAC      50
   GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
   TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
   ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGACTGGGGT      200
   TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
55  TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
   GAACAAGCAC ACCTGTCTAC AACTGGGGATA GAGCATATTT CGGTAATATT      350
   ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
   TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
   GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTT AAGTAATACA      500
60  ACAGAACTA ATAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550

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	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTIONACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214

15

2) INFORMATION FOR SEQ ID NO: 1010

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-07

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACTTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTIONGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTGTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTC	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

60

2) INFORMATION FOR SEQ ID NO: 1011

- (i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 1207 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

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AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA ATACGTCTCT      50
TACCCTGACG ATGATTGCA AGTCGCATCT ACGGTCGTAG ATGTTTCAAA      100
20 TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA AGTAACGTTT      150
CATTGTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG GGGTTCTGCT      200
ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG GTGTTTATGA      250
TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT CCGGGAACAA      300
GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTCCGTAA TATTACTCTG      350
25 CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG AGACTTTGAA      400
TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT CTTGGTATCG      450
ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA TACAACAGAA      500
TCTATAAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG CTGCTTATGC      550
TGCCTTTGCA AATGGTGCCA CTTACTATAA ACCAATGTAT ATCCATAAAG      600
30 TCGTCTTCAG TGATGGAAGT AAAAAAGAGT TCTCTAATGT CGGAACTCGT      650
GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA TGAAAACAGT      700
CTTGACTTAT GGAACCTGGC GTGGAGCCTA TCTTCCTTGG CTTCTCAAG      750
CTGGTAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT TGAAAACCAC      800
ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG TTGGTTATAC      850
35 TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCGAAT CGTTTAACTC      900
CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA TCGCTCAATG      950
ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA CGATGCCAGA      1000
CGGACTTTTC AGAAACGGGG AATTGTGATT CAAAAATGGA GCTCGCCCAA      1050
TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA AAGTTCAAGC      1100
40 TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA CTCCAAGCAC      1150
AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA CAATCAAATA      1200
CAACCCC                                           1207

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45

2) INFORMATION FOR SEQ ID NO: 1012

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
20	CTATCGTTTG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATG	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGAACCT	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTCCGTA	CCAACCAGGC	CGTAGAAACC	AATCGTGACT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGACT	ATGCTCCCGC	TTTAGAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACAACCTG	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	500
	ACACAACCTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GACTGAAATG	700
60	ATGAAAACCTG	TTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAACTATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAACT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAAA	TGCCATTTC	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	TCCACAACA	ACCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

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2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 bases

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- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTA	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATAC	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

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2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTA	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAA	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACCTG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACCTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCCTACGC	TGCTTTTGTG	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACCTGT	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGT	TCATCATCAG	ATAGTTCAAC	TTACACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1229 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 35 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGA	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGCT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACCTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACCTCAACC	1150
	ACTCCAAGCA	CAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCC	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAAC	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCAC	ACTCAAATGC	TATTTCAAGT	500
35	AATACAAC	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCT	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTA	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACCTGGCTAC	GTAAGTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAGT	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
50	AACAATCAA	TACAACCCCT	GATCA			1225

2) INFORMATION FOR SEQ ID NO: 1019

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 5 (B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

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10 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTTGGAACC TCCTATTTGG AAAAGCAATA      200
   TGAAGAGACC TTACAAGGAA AACGCTCGGT AAAAGAAATC CATCTGGATA      250
   AATATGGCAA TATGGAAAGC GTGGACACAA TTGAGGAAGG TAGTAAGGGA      300
15 AACAATATCA AACTGACCAT TGATTTGGCC TTCCAAGATA GCGTGGATGC      350
   TTTGCTGAAA AGTTATTTCA ATTCCGAGCT AGGAAATGGT GGAGCTAAAT      400
   ATTCTGAAGG TGTCTATGCA GTCGCCCTTA ACCCAAAAAC AGGTGCTGTT      450
   TTATCCATGT CAGGGATCAA ACATGACCTG AAAACGGGAG AGTTGACTCC      500
   TGATTCCTTG GGAACGGTAA CCAATGTCTT TGTCCCAGGT TCGGTTGTCA      550
20 AGGCTGCGAC CATCAGCTCA GGTGCGGAAA ATGGTGTTTT ATCAGGAAAC      600
   CAAACCTTAA CAGATCAGCC TATTGTTTTT CAAGGTTTCA CTCCAATTTA      650
   TTCTTGGTAT AAATTGGCAT ATGGATCTTT TCCTATTACA GCTGTGGAAG      700
   CCTTGAGTA TTCATCCAAT GCTTACATGG TTCAAACCGC TCTTGGAATC      750
   ATGGGCCAGA CCTATCAACC AAATATGTTT GTTGAACCA GCAATTTGGA      800
25 AACAGCTATG GGAAACTTC GTGCGACCTT TGGCGAATAT GGCTTGGGGG      850
   CTGCGACCGG AATTGACCTA CCAGATGAAT CTACTGGATT TGTTCCCAAA      900
   GAGTATAGCT TTGCTAATTA CATCACCAAT TCCTTTGGGC AGTTTGATAA      950
   CTATACGCCC ATGCAGTTGG CTCAGTATGT AGCAACTATT GCAAATAATG     1000
   GTGTTCTGTT GGCCTCCTCGT ATTGTTGAAG GCATTTATGG TAATAATGAT     1050
30 AAGGGAGGAC TGGGTGACTT GATTTCAGCA CTGCAACCGA CAGAGATGAA     1100
   TAAGGTCAAT ATATCCGACT CCGATATGAG CATCTTGCAC CAAGGTTTTT     1150
   ATCAGGTTGC CCATGGTACT AGTGGATTGA CAACTGGACG TGCCTTTTCA     1200
   AATGGTGCCT TGGTATCCAT TAGCGGAAAA ACAGGTACAG CCGAAAGCTA     1250
   TGTGGCAGAT GGTCAGCAAG CAACCAATAC CAATGCGGTG GCCTATGCCC     1300
35 CATCTGATAA TCCCCAAATC GCTGTGCGAG TGGTCTTTCC TCATAATACC     1350
   AATCTAACAA ATGGTGTAGG ACCTTCCATT GCGCGTGACA TTATCAATCT     1400
   GTATCAAAAA TACCATCCAA TGAAGTAGAA AGGAAATTA      1439

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2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

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60 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTTGGAACC TCCTATTTGG AAAAGCAATA      200

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	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCCTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGAGATA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAACTTTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAAATAATG	1000
	GTGTTCTGT	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTTCAGCA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCC	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCCGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

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2) INFORMATION FOR SEQ ID NO: 1022

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1428 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTTC	AAGGTTTCAG	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGGAGTAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACCAG	CAATTTGGAA	ACAGCTATGG	800
	GAAAACCTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTTCGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGACAC	AAGGTTTTTA	TCAGGTGACC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTGCGAGT	GGTCTTTCC	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT	TCAAAGGAGA	TGCCTGGCAT	TAGTATTTCT	ACTTCTTG	50
	ATCGAAAGGT	TTTGGAAACT	TCCCTTTCTT	CTATAGTAGG	GAGTGTATCC	100
	AGTGAAAAAG	CTGGTCTCCC	AGCGGAAGAA	GCAGAATCCT	ATCTTAAAAA	150
	AGGCTATTCT	CTAAATGACC	GTGTTGGAAC	CTCCTATTTG	GAAAAGCAAT	200
	ATGAAGAGAC	CTTACAAGGA	AAACGCTCGG	TAAAAGAAAT	CCATCTGGAT	250
25	AAATATGGCA	ATATGGAAAG	CGTGGACACA	ATTGAGGAAG	GTAAGTAAAGG	300
	AAACAATATC	AAACTGACCA	TTGATTTGGC	CTTCCAAGAT	AGCGTGGATG	350
	CTTTGCTGAA	AAGTTATTTT	AATTCCGAGC	TAGGAAATGG	TGGAGCTAAA	400
	TATTCTGAAG	GTGTCTATGC	AGTCGCCCTT	AACCCAAAAA	CAGGTGCTGT	450
	TTTATCCATG	TCAGGGATCA	AACATGACCT	GAAAACGGGA	GAGTTGACTC	500
30	CTGATTCCTT	GGGAACGGTA	ACCAATGTCT	TTGTCCCAGG	TTCCGGTTGTC	550
	AAGGCTGCGA	CCATCAGCTC	AGGTTGGGAA	AATGGTGTTT	TATCAGGAAA	600
	CCAAACCTTA	ACAGATCAGC	CTATTGTTTT	CCAAGGTTCA	GCTCCAATTT	650
	ATTCTTGGTA	TAAATTGGCA	TATGGATCTT	TTCCTATTAC	AGCTGTGGAA	700
	GCCTTGGAGT	ATTCATCCAA	TGCTTACATG	GTTCAAACCG	CTCTTGAAT	750
35	CATGGGCCAG	ACCTATCAAC	CAAATATGTT	TGTTGGAACC	AGCAATTTGG	800
	AAACAGCTAT	GGGAAAACTT	CGTGCGACCT	TTGGCGAATA	TGGCTTGGGG	850
	GCTGCGACCG	GAATTGACCT	ACCAGATGAA	TCTACTGGAT	TTGTTCCCAA	900
	AGAGTATAGC	TTTGCTAATT	ACATCACCAA	TTCTTTGGG	CAGTTTGATA	950
	ACTATACGCC	CATGCAGTTG	GCTCAGTATG	TAGCAACTAT	TGCAAATAAT	1000
40	GGTGTTTCGT	TGGCTCCTCG	TATTGTTGAA	GGCATTATATG	GTAATAATGA	1050
	TAAGGGAGGA	CTGGGTGACT	TGATTCAGCA	ACTGCAACCG	ACAGAGATGA	1100
	ATAAGGTCAA	TATATCCGAC	TCCGATATGA	GCATCTTGCA	CCAAGGTTTT	1150
	TATCAGGTTG	CCCATGGTAC	TAGTGGATTG	ACAACTGGAC	GTGCCTTTTC	1200
	AAATGGTGCC	TTGGTATCCA	TTAGCGGAAA	AACAGGTACA	GCCGAAAGCT	1250
45	ATGTGGCAGA	TGGTCAGCAA	GCAACCAATA	CCAATGCGGT	GGCCTATGCC	1300
	CCATCTGATA	ATCCCCAAAT	CGCTGTCGCA	GTGGTCTTTC	CTCATAATAC	1350
	CAATCTAACA	AATGGTGTAG	GACCTTCCAT	TGCGCGTGAC	ATTATCAATC	1400
	TGTATCAAAA	ATACCATCCA	ATGAACTAGA	AAGGAAATTA	TG	1442

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2) INFORMATION FOR SEQ ID NO: 1024

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTGGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTATCCAT	GTCAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCC	TGGGAACGGT	AACCAATGTC	TTTGTCCAG	GTTCCGGTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGTGT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACCA	ATTCCTTTGG	GCAGTTTGAT	950
	AACTATACAC	CCATGCAGTT	GGCTCAGTAT	GTCAGCAACTA	TTGCAAAATA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTTCAG	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTGCG	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAAC TAG	AAAGGAAATT	ATGCT	1445

40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

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	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGA	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTGG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCTT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGT	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTC	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AACTATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAAATGA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTGAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCTT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACGTGTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441
25						

2) INFORMATION FOR SEQ ID NO: 1026

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-08
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGTTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAACATGTA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTCCGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1029

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

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575

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATAGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTTCCAG	GTTCCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGACCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTT	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTGG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAAATGA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAAG	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACTGGC	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1447 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

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	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAAATA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCTTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
25	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGCT	1447

2) INFORMATION FOR SEQ ID NO: 1031

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1446 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCTTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTTGGAA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTGTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GA CTGGGTGA	CTTGATT CAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAAC TA	GAAAGGAAAT	TATGCT	1446

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2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAA	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTGTGTTCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACTATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATT CAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CCTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGTTGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1034

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

	GGAAACTGCA	GAGGTCAAGG	GGATTGATTT	TACAACCAGT	CCCAATCGTA	50
	GTTATCCAAA	CGGACAATTT	GCTTCTAGTT	TTATCGGACT	AGCTCAGCTC	100
10	CATGAAAATG	AAGATGGCAG	CAAGAGCTTA	CTGGGAACCT	CTGGAATGGA	150
	GAGTTCCTTG	AACAGTATTC	TTGCAGGGAC	AGACGGTATT	ATTACCTATG	200
	AAAAAGACCG	TGTAGGAAAT	ATCGTACCAG	GTACAGAACT	GGTATCGCAA	250
	CAAACTGTGG	ATGGCAAGGA	TGTTTATACA	ACATTGTCTA	GTCCGCTACA	300
	ATCTTTCATG	GAAACTCAGA	TGGATGCCTT	TCTAGAAAAA	GTAAAAGGTA	350
15	AGTATATGAC	CGCGACCTTG	GTCAGTGCAA	AGACCGGTGA	AATCCTCGCT	400
	ACCACCCAAC	GACCTACCTT	TAATGCAGAT	ACTAAAGAAG	GAATCACTGA	450
	GGACTTTGTT	TGGCGTGATA	TTCTTTATCA	AAGTAACTAT	GAACCAGGAT	500
	CAGCCATGAA	GGTTATGACG	TTAGCTTCTT	CTATTGATAA	TAATACCTTC	550
	CCAAGTGGAG	AATACTTCAA	TAGCAGTGAA	TTCAAAATAG	CGGATGCGAC	600
20	GACTCGAGAT	TGGGATGTTA	ATGATGGTTT	GACTACTGGT	GGGATGATGA	650
	CTTTCTTACA	AGGTTTTCGCT	CACTCCAGTA	ATGTTGGAAT	GAGTCTACTT	700
	GAACAAAAAA	TGGGAGATGC	TACTTGGTTG	GATTATCTAA	AACGCTTTAA	750
	ATTTGGGGTT	CCAACCTCGCT	TTGGCTTGAC	AGATGAATAC	GCTGGTCAAC	800
	TTCCAGCTGA	TAATATTGTT	AGTATTGCTC	AAAGCTCATT	TGGGCAAGGA	850
25	ATTTCACTGA	CACAAACACA	AATGCTTCGT	GCCTTTACAG	CTATTGCTAA	900
	TGATGGAGTT	ATGCTGGAGC	CAAAATTTAT	AAGTGCTATT	TATGATACTA	950
	ACAATCAGTC	TGTACGTAAG	TCACAAAAAG	AAATAGTAGG	AAATCCTGTT	1000
	TCCAAAGAGG	CAGCAAGCAC	AACTCGAAAT	CACATGATCT	TAGTTGGGAC	1050
	GGACCCCTCTA	TATGGAACTA	TGTATAATCA	CTACACAGGA	AAGCCAATTA	1100
30	TAACAGTTCC	TGGACAAAAT	GTAGCAGTTA	AATCCGGTAC	GGCTCAAATC	1150
	GCTGATGAGA	AAAATGGAGG	ATACTTGGTT	GGTTCTACCA	ATTATATTTT	1200
	CTCAGTTGTG	ACTATGAATC	CTGCTGAAAA	TCCTGATTTT	ATCTTGATATG	1250
	TAACGGTTCA	ACAGCCTGAG	CATTATTCAG	GTATCCAGTT	GGGAGAATTT	1300
	GCCACCCCAA	TCTTGGAGCG	GGCTTCAGCT	ATGAAAGAAT	CTCTCAATCT	1350
35	TCAATCTCCA	GCCAAAAATT	TAGATAAAGT	TACGACAGAA	TCTTCTTATG	1400
	CAATGCCTAG	CATCAAGGAT	ATTTACCTTG	GTGAGTTGGC	GGAAGCCTTA	1450
	CGCCGAAATA	TTGTGCAACC	AATCGTTGTA	GGTACTGGAA	CAAAGATTAA	1500
	AGAGACTTCT	GTAGAAGAAG	GGACCAATCT	TGCACCAAAC	CAACAAGTTC	1550
	TCCTTTTATC	GGATAAGGTA	GAAGAAATTC	CAGACATGTA	TGGCTGGAAA	1600
40	AAAGAGACTG	CCGAGACCTT	TGCTAAATGG	TTGGATATTG	AACTGGAATT	1650
	TGAAGGTTCA	GGTTCCGTTG				1670

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1683 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

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	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCCCTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	CGGTGATATT	CTTTATCAAA	GTAACATATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	TGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAAGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTTCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
	CTGGAATTTG	AAGGTTTCAG	TTCCGTTGTT	CAG		1683
35						

2) INFORMATION FOR SEQ ID NO: 1036

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-03
- 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGCAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAACGCTT	TAAATTTGGG	GTTCCAACCT	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCTT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGG	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TTTCTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAACCTGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAAGTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
5	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCTT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAAAT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAGTGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA		1685

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2) INFORMATION FOR SEQ ID NO: 1039

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1679 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
	GTATCGCAAC	AACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTCAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGTTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGATATG	AACGGTTCAA	CAGCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGGTTTCAG	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAACCTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTTCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAAC TGGA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

20	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTAACATATG	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGTTTGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGTTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAGAAG	1696

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2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCCCTC	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCACTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCCTC	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAA	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATT	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACTTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

- (A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

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5  CAAAAAAGAG TTGGAAACTG CAGAGGTCAA GGGGATTGAT TTTACAACCA      50
   GTCCTAATCG TAGTTACCCA AACGGACAAT TTGCTTCTAG TTTTATCGGT      100
   CTAGCTCAAC TCCATGAAAA TGAAGATGGA AGCAAGAGTT TGCTGGGAAC      150
   TTCTGGAATG GAGAGTTCCT TGAACAGTAT TCTTGCAGGG AAAGACGGTA      200
   TTATTACTTA TGAAAAGGAT CGTCTGGGTA ATATTGTCCC TGGAACAGAA      250
10  CAAGTTTCCC AACAAACGGT AGATGGCAAG GATGTTTATA CAACATTGTC      300
   TAGTCCGCTC CAATCTTTCA TGGAAACTCA GATGGATGCC TTTCTAGAAA      350
   AAGTAAAAGG TAAGTATATG ACCGCGACCT TGGTCAGTGC AAAGACCGGT      400
   GAAATCCTCG CTACCACCCA ACGACCTACC TTTAATGCAG ATACTAAAGA      450
   AGGAATCACT GAGGACTTTG TTTGGCGTGA TATTCTTTAT CAAAGTAACT      500
15  ATGAACCAGG ATCAGCCATG AAGGTTATGA CGTTAGCTTC TTCTATTGAT      550
   AATAATACCT TCCCAAGTGG AGAATACTTC AATAGCAGTG AATTCAAAT      600
   AGCGGATGCG ACGACTCGAG ATTGGGATGT TAATGATGGT TTGACTACTG      650
   GTGGGATGAT GACTTTCTTA CAAGGTTTCG CTCACTCCAG TAATGTTGGA      700
   ATGACTGTAC TTGAACAAAA AATGGGAGAT GCTACTTGGT TGGATTATCT      750
20  AAAACGCTTT AAATTTGGGG TTCCAACCTG CTTTGGCTTG ACAGATGAAT      800
   ACGCTGGTCA ACTTCCAGCT GATAATATTG TTAGTATTGC TCAAAGCTCA      850
   TTTGGGCAAG GAATTTTCAGT GACACAAACA CAAATGCTTC GTGCCTTTAC      900
   AGCTATTGCT AATGATGGAG TTATGCTGGA GCCAAAATTT ATAAGTGCTA      950
   TTTATGATAC TAACAATCAG TCTGTACGTA AGTCACAAAA AGAAATAGTA     1000
25  GGAAATCCTG TTTCCAAAGA GGCAGCAAGC ACAACTCGAA ATCACATGAT     1050
   CTTAGTTGGG ACGGACCCTC TATATGGAAC TATGTATAAT CACTACACAG     1100
   GAAAGCCAAT TATAACAGTT CCTGGACAAA ATGTAGCAGT TAAATCCGGT     1150
   ACGGCTCAAA TCGCTGATGA GAAAAATGGA GGATACTTGG TTGGTTCTAC     1200
   CAATTATATT TTCTCAGTTG TGACATGAA TCCTGCTGAA AATCCTGATT     1250
30  TTATCTTGTA TGTAACGGTT CAACAGCCTG AGCATTATTC AGGTATCCAG     1300
   TTGGGAGAAT TTGCCACCCC AATCTTGGAG CGGGCTTCAG CTATGAAAGA     1350
   ATCTCTCAAT CTTCAATCTC CAGCCAAAAA TTTAGATAAA GTTACGACAG     1400
   AATCTTCTTA TGCAATGCCT AGCATCAAGG ATATTTTACC TGGTGAGTTG     1450
   GCGGAAGCCT TACGCCGAAA TATTGTGCAA CCAATCGTTG TAGGTACTGG     1500
35  AACAAAGATT AAAGAGACTT CTGTAGAAGA AGGGACCAAT CTTGCACCAA     1550
   ACCAACAAAGT TCTCCTTTTA TCGGATAAGG TAGAAGAAAT TCCAGACATG     1600
   TATGGCTGGA AAAAAGAGAC TGCCGAGACC TTTGCTAAAT GGTTGGATAT     1650
   TGAAGTGGAA TTTGAAGGTT CAGGTTCCGT TGTTTCAAGG     1690

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2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

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AGTTGGAAAC TGCAGAGGTC AAGGGGATTG ATTTTACAAC CAGTCCTAAT      50
CGTAGTTACC CAAACGGACA ATTTGCTTCT AGTTTTATCG GACTAGCTCA      100
60  GCTCCATGAA AATGAAGATG GCAGCAAGAG CTTGCTGGGA ACCTCTGGGA      150

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	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGBAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTCT	AGATTGGGAT	GTAAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTC	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAACTG	TTCTTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAACGG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGCACC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATCCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG			1680

2) INFORMATION FOR SEQ ID NO: 1046

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TAAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAAGTGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCAGAAG		1689

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2) INFORMATION FOR SEQ ID NO: 1047

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTTC	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTCC	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTCAGC	GACCCAGACG	CAAATGATTC	GTGCCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAAGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGAA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTACCC	TGGCGATTTG	1450
	GCGGAAGCCT	TACGTCGCAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGCACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAAGTC	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTC	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAAGTAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTTCA	GTTCCGTCGT	TC		1682

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2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1241 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R690

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
25	GGTTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	150
	CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	200
	AATCTGGTGT	ATGGAAAAATG	TGCGAAAAAC	CTTGCGCGGA	250
	GACAATTGCT	ATTCAGCTGT	ACTCTCGCCG	GATAAAAAAA	300
	ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	350
30	TTTCAGCTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	400
	TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	450
	AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	500
	TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	550
	GCTACGTTTA	CCTATCCTGT	TTTTGTAAAG	CCGGCGCGTT	600
35	CTTCGGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	650
	AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	700
	GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	750
	TGGCGAGGTG	GACCAATCA	GGCTGCAGTA	CGGAATCTTT	800
	AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	850
40	GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	900
	AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	950
	TACAAGATAA	CGGCCGCATT	GTACTGAACG	AAGTCAATAC	1000
	TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	1050
	ACTTCCCGAA	CTGATTGACC	GCTTGATCGT	ATTAGCGTTA	1100
45	AAGCATGGAA	ATAGGATTTA	CTTTTTTAGA	TGAAATAGTA	1150
	GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTTACCCGG	1200
	GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	1241
				T	

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2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCCGTGTG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTCT	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

50	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGA AAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTTAGAT	GAAATAGTAC	1150
	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTGAA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGA AAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237